

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 10:53:51 ; Search time 166 Seconds

(without alignments)
687.836 Million cell updates/sec

Title: US-08-989-881-2

Perfect score: 1419

Sequence: 1 MANQTQSDXKVLGRELGRG.....TKRLTAQQVLDHPWQNAKK 274

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1859788 seqs, 416717961 residues

Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

```

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1419	100.0	274	15	US-10-425-114-70054
2	1318	92.9	274	15	US-10-425-114-70054
3	1252	88.2	536	15	US-10-424-599-180685
4	1246	87.8	535	15	US-10-425-114-45800
5	1164	82.0	533	15	US-10-424-599-200299
6	1155	81.4	550	15	US-10-437-963-109887
7	1147	80.8	553	15	US-10-425-114-68288
8	1143	80.5	539	16	US-10-425-115-213591
9	1143	80.5	553	15	US-10-425-114-67473
10	1136	80.1	538	16	US-10-425-115-198373
11	1136	80.1	592	15	US-10-425-114-65930

```

12 1136 80.1 592 15 US-10-425-114-70054
13 1135 80.0 425 16 US-10-767-701-44784
14 1132 79.8 589 16 US-10-437-963-160820
15 1115 78.6 661 16 US-10-437-963-163957
16 1101 77.6 541 16 US-10-425-114-57084
17 1084 76.4 612 16 US-10-437-963-199098
18 1064.5 75.0 531 16 US-10-425-115-231166
19 1064.5 75.0 540 15 US-10-425-114-49937
20 1064.5 75.0 545 15 US-10-425-114-49391
21 1062 74.8 465 15 US-10-425-114-59388
22 1048 73.9 503 16 US-10-437-963-186792
23 1041 73.4 563 16 US-10-437-963-186792
24 1018.5 71.8 535 15 US-10-424-599-254375
25 947 66.7 549 9 US-09-828-313-39
26 947 66.7 549 16 US-10-768-8638-39
27 932 65.7 595 16 US-10-437-963-141791
28 926 65.3 470 15 US-10-425-114-70198
29 926 65.3 639 9 US-09-854-731-17
30 926 65.3 640 16 US-10-425-115-340679
31 916 64.6 413 15 US-10-243-5818-2
32 916 64.6 612 16 US-10-437-963-139689
33 914.5 64.4 578 16 US-10-437-963-134013
34 910 64.1 513 16 US-10-437-963-173217
35 910 64.1 546 15 US-10-424-599-203557
36 910 64.1 549 15 US-10-425-114-54704
37 910 64.1 583 15 US-10-425-114-45048
38 909.5 64.1 518 16 US-10-437-963-168927
39 906 63.8 582 16 US-10-425-115-228630
40 900 63.4 341 16 US-10-437-963-161238
41 899 63.4 355 16 US-10-767-701-45463
42 898 63.3 549 16 US-10-437-963-164372
43 897 63.2 568 16 US-10-437-963-204568
44 896.5 63.2 577 16 US-10-437-963-131419
45 896 63.1 578 16 US-10-437-963-111277

```

ALIGNMENTS

```

RESULT 1
US-10-243-581B-1
; Sequence 1, Application US/10243581B
; Publication No. US20030219763A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Plant Protoplast Gene Expression Systems
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 00786/386002
; CURRENT APPLICATION NUMBER: US/10/243,581B
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/US01/07999
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,074
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 08/989,881
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 60/032,966
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: US 09/371,338
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/095,938
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-243-581B-1

```

Query Match 100.0%; Score 1419; DB 15; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.3e-108;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MANOTQSDKVIILGRELGRGFBGITYLCTDRETRREALACKSISKRLRTAVDVEDVRVV	60
Db	1	MANOTQSDKVIILGRELGRGFBGITYLCTDRETRREALACKSISKRLRTAVDVEDVRVV	60
Qy	61	TIMSTLPEHPNVVKLKATYEDNETVHLMELCEGGELFGRIIVARGHYTERAAATVARTIA	120
Db	61	TIMSTLPEHPNVVKLKATYEDNETVHLMELCEGGELFGRIIVARGHYTERAAATVARTIA	120
Qy	121	EVVRMCHVGMVHRDLKPENFLFANKENSALKAI DFGLSVLPKPERFETVGSPPYMA	180
Db	121	EVVRMCHVGMVHRDLKPENFLFANKENSALKAI DFGLSVLPKPERFETVGSPPYMA	180
Qy	181	PEVLKRNYPGEVDVMSAGVIYIILLCGVPPFPAETEQGVALLA ILRGVLD FKRPDQWSQISE	240
Db	181	PEVLKRNYPGEVDVMSAGVIYIILLCGVPPFPAETEQGVALLA ILRGVLD FKRPDQWSQISE	240
Qy	241	SAKSLVKOMLPDSTFKRLTAQOVLDPHPMIONAKK	274
Db	241	SAKSLVKOMLPDSTFKRLTAQOVLDPHPMIONAKK	274

RESULT 2

```

US-10-243-581B-3
; Sequence 3, Application US/10243581B
; Publication No. US20030219763A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Plant Protoplast Gene
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 00786/386002
; CURRENT APPLICATION NUMBER: US/10/243,581B
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/US01/07999
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,074
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 08/989,881
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 60/032,966
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: US 09/371,338
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/095,938
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-243-581B-3

```

Query Match	Score 1318;	DB 15;	Length 274;
Best Local Similarity	92.0%;		
Matches 252;	Conservative	8;	Mismatches 14;
			Indels 0;
			Gaps 0;

[illegible]

```

Qy      241 SAKSLVKQMLPDSPTKRLTAQOVLDDHPWIONAXK 274
          |||||:::||::|||
Db      241 SAKSLVKQMLDPDPTKRLTAQOVLAAHPWIONAXK 274
          |||||:::||::|||

RESULT 3
US-10-424-599-180685
; Sequence 180685, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules an
; TITLE OF INVENTION: Plants and Uses Thereof for
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 180685
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(536)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134173C
US-10-424-599-180685
```

	Query Match	88.2%	Score 1252;	DB 15;	Length 536;
	Best Local Similarity	86.1%;	Pred. No. 1.6e-94;		
	Matches 236; Conservative	17;	Mismatches 21;	Indels 0;	Gaps 0;
Qy	1	MANOTQISDKYILGRELGRGFGITYLCTDREYREALACKSISKRKLRTAVDVEDVRREV	60		
Db	47	VTSRLGDKYVIGRELGRGFGITYLCTDREYKQELACKSISKRKLRTAIDVEDVRREV	106		
Qy	61	TIIMSTLPEHPNVVKLKATYEDNETVHLVMBELCGGELFGRIVARGHYTERAAATVARTIA	120		
Db	107	AIMSTLPEHANVVKLKATYEDNEENVHVLMBELCAGGELFDRIVARGHYSERAAANVARTIA	166		
Qy	121	EVVRMCHVNGVMHRDLKPENFLPANKKENSALKAIIDFGLSVLPKPGGRPFTEIVGSPYMA	180		
Db	167	EVVRMCHANGVMHRDLKPENFLPANKKENSVLKAIIDFGLCVFFPIPGGRFTEIVGSPYMA	226		
Qy	181	PEVLKKNYGPEDVWWSAGVITYILLCGVPPFWAEIQGVALAILRGVLDFKRDPMWSQISE	240		
Db	227	PEVLKKNYGPEDVWWSAGVITYILLCGVPPFWAFAFQGVALAILRGVLDFKREWPQISE	286		

```

RESULT 4
US-10-425-114-45800
; Sequence 45800, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecule
; TITLE OF INVENTION: Plants and Uses There
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28

```

```

; NUMBER OF SEQ ID NOS: 73128
;
; SEQ ID NO 45800
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Glycine max
;
; FEATURE:
; OTHER INFORMATION: Clone ID: 700989873_Flt.pep
US-10-425-114-45800

```

```
Query Match      87.8%; Score 1246; DB 15; Length 555;
Best Local Similarity 85.8%; Pred. No. 5.1e-94;
Matches 235; Conservative 19; Mismatches 20; Indels 0; Gaps 0
```

Qy	1	MANQTOISDKYILGRELGRGFGITYLCTDRETRREALACKSISKRLRTAVDVEDVREV	60
Db	63	VTSRSLIGDKYVIGRELGRGFGITYLCTDRETKQELACKSISKRLRTAIDVEDVREV	122
Qy	61	TIMSTLPHPNVVKLKAITYEDONETVHLMELCEGELFGRIIVARGHYTERAAATVARTIA	120
Db	123	AIMSTLPEHANVVKLKAITYEDBENVHLMELCAGELPDRIIVARGHYSERAAANVARTIA	182
Qy	121	EVWRMCHVNGVWHRDLKPENFLPANKKENSALKAI DFGLSVLPKGERPTEIVGSPYMA	180
Db	183	EVWRMCHANGVWHRDLKPENFLPANKKENSVLKAI DFGLSVFEPKGERPSEIVGSPYMA	242
Qy	181	PEVLKRNYPGEVDVWSAGVILYLICGVPFPWAETEQGVVALAILRGVLDPFKDPPMSQISE	240
Db	243	PEVLKRNYPGEVDVWSAGVILYLICGVPFPWAEDERGVALAILRGVDFKKEPWPQISD	302
Qy	241	SAKSILVKOMLBPFDSTKRITAAQOVLDPHPMIQNAKK	274
Db	303	SAKSILVROWLEHDPKKRITAEQVLSHSMIQNAKK	336

```

RESULT 5
US-10-424-599-200299
; Sequence 200299, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 200299
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_22897C.1.pep
US-10-424-599-200299

```

Query Match 82.0%; Score 1164; DB 15; Length 533;
Best Local Similarity 81.0%; Pred. No. 2.7e-87;
Matches 217; Conservative 24; Mismatches 27; Indels 0; Gaps 0

QY	7	ISDKYILRELGRGFBGITYLCTDRETRREALACKSISKRKLRTAVDVEDVREVTIMSTL	66
DB	55	IEDRYLVRELGRGFBGVLYLCIDRDRRELLACKSISKRKLRTAVDVEDVREVALMRHL	114
QY	67	PEHPNVKLIKATYEDNETVHLMVLCGEGELFGRIIVARGHYTERRAAATVARTIAEVRMC	126
DB	115	PESPSIVSLREACEDDNAVHLMVLCGEGELFERIIVARGHYTERRAAAATRTTIVVQJLC	174
QY	127	HWNGVWHRDLKPENFLFANKKNSALKATDFGLSVLFPKGPFRTEIVGSPYMAPEVLKR	186
DB	175	HKHGVIHRDLKPENFLFANKKNSPLKATDFGLSIFPKGPFRSEIVGSPYMAPEVLKR	234

QY	187	NYGPEVDVWSAGVITYLILCCGPPFPAETEGVVALAILGURGVLDKFKRDPSQISESAKSILV	244
Db	235	NYGPEIDIWSAGVITYLILCCGPPFPAESEQVQAAILRGLIDFKKEPWPISSESAKSILV	294
QY	247	KQMLEPDSTKRLTATACQVLDHPWIIQNAKK	274
Db	295	RQMLEPDPPKRLRTAKQVLEHPWIIQNAKK	322

```

RESULT 6
US-10-437-963-109887
; Sequence 109887, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid M
; TITLE OF INVENTION: Plants and Uses Th
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,9
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109887
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT45
; US-10-437-963-109887

```

Query Match	81.4%	Score 1155	DB 16	Length 550
Best Local Similarity	80.6%	Pred. No. 1.6e-86		
Matches 216	Conservative 22	Mismatches 30	Indels 0	Gaps 0
Qy	7	ISDKYILGRGREGFGITYLCTDRETRALACKSISKRKLTAVDVEDVRREVTIMSTL	66	
Db	71	IAARYLGGELGRGREGFGVTYLTCTERTGDVACKSISKKKLTAVDIEDVRREVDIRHL	130	
Qy	67	PEHPNVVKLKATYEDNEVHVLVMELCGEGELFGRIVARGHYTERAAATVARTIAEVVRC	136	
Db	131	PKHPNIVTLRTYEDDNAVHVLVMELCGEGELFDRIVARGHYTERAAALVTRIVEVQMC	190	
Qy	127	HVNGVMHRDLKPENFLPANKKENSALKAI DFGLSVLPKPGERTFTIVSGSPYYMAPVLKR	186	
Db	191	HKHGVMRDLKPENFLPANKKETAALKAI DFGLSVFFTPGERFTFTIVSGSPYYMAPVLKR	250	
Qy	187	NYGPEVDVWSAGVILYILLCGVPPPWASTEQQVALAILRGVLDFKRPDPWSQISESAKSLV	246	
Db	251	NYGPEVDVWSAGVILYILLCGVPPPWASTEQQVAQIIIRSVLIDFKRPDPWRVSDNAKDLV	310	
Qy	247	KOMLEPDSTKRLTAQQVLDPHPIQNAKK	274	
Db	311	KGMLNPDPERRLNAAQVLDHPWLQNIKK	338	

RESULT 7
US-10-425-114-68288
; Sequence 68288, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```

QY      127   HVGVMHRDLKPENFLFANKKENSALKAIDFGLSVLFKPGBRFTTEIVGSPYYMAPEVLKR 186
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      180   HKHGVMRDLKPENFLFANKKESAAALKAIDFGLSVFFTPGERFSEIVGSPYYMAPEVLKR 239
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      187   NYGPEVDWWSAGVILTYILLCCVPFPFWAETEGVALAILRLGVLDPKRDPWSOISESAKSILV 246
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      240   NYGPEVDWWSAGVILTYILLCCVPFPFWAETEGOVAQAIRSIDFKRDPWPVRSDNAKOLV 299
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      247   KQMLEPDSRTKRLTAQQVLDPHPWIQNAKK 274
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      300   RGMNLNPDPKRLRTAHQVLGHFWLQNIKK 327
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-10-425-114-67473
; Sequence 67473, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67473
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4757-010-H10_FU1.pep
US-10-425-114-67473

```

Query Match	80.5%;	Score 1143;	DB 15;	Length 553;
Best Local Similarity	80.2%;	Pred. No. 1.5e-85;		
Matches 215;	Conservative 23;	Mismatches 30;	Indels 0;	Gaps 0;
Qy	7	ISDKYILGRELGRGEGITVLCYDRETRREALACKSISKRLRTAVDVEDVRREVTIMSTL	66	
Db	74	IAARYELGAEGLRGEGVTYLCYDTRASGEALACKSISKRLRTAVDLEDVRREVEIMRHL	133	
Qy	67	PEHPNVVVKATYEDNETVHLMVELCEGGBELFGRIVARGHYTERAAATVARTIAEVRMC	126	
Db	134	PKHPNVVTLRTDYEDDNAVHLMVELCEGGBELFGRIVARGHYTERAAALVLTIVVQMC	193	
Qy	127	HVNGVMHRDLKPNFLFANKKENSALKAIDFGLSVLFPKGERFTEIVGSPYYMAPEVLKR	186	
Db	194	HKHGVNHRDLKPNFLFANKKESAAALKAIDFGLSVFTPGERFSEIVGSPYYMAPEVLKR	253	
Qy	187	NYGPEVDVWSAGVILYILLCGVPPFWAETEGQVALAILRGVLDPFKRPDPWSQISAKSLV	246	
Db	254	NYGPEVDVWSAGVILYILLCGVPPFWAETEGQVAQAIIRSVIDFKRPDPWPVRVSDNAXDLV	313	
Qy	247	KQMLEPDSYTKRLTAQOVLDPHPWTQNAKK	274	
Db	314	RGLNLPDPPKRLTAHVLGHVLPWTQNTKK	341	

RESULT 10
US-10-425-115-198373
; Sequence 198373, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With


```
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 198373
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Zea mays
; NAME/KEY: unsure
; LOCATION: (1)..(538)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112494C.1.pep
; US-10-425-115-198373

Query Match      80.1%; Score 1136; DB 16; Length 538;
Best Local Similarity 79.1%; Pred. No. 5.6e-85;
Matches 212; Conservative 26; Mismatches 30; Indels 0; Gaps 0;

Qy 7 ISDKYILGRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 66
Db 58 IDDKYVLDRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 117

Qy 67 PEHPNVVKLKATYEDNETVHLMELCEGGELFGRIVARGHYTERAAATVARTIAEVVRMC 126
Db 118 PKSPSVVSLREACDDGAVHLVMECEGGELFGRIVARGHYTERAAASVTRTILEVVOLC 177

Qy 127 HVGVMHRDLKPENFLFANKKENSALKADIFGLSVLPKPGERFTEIVGSPYYMAPEVLKR 186
Db 178 HRHGVHHRDLKPENFLFANKKENSPLKADIFGLSIFPKGKEKFEIVGSPYYMAPEVLKR 237

Qy 187 NYGPEVDVMSAGVILYILLCGVPPFWAETEGQVALAILRGVLDPKRDPWQSOISSAKSLV 246
Db 238 NYGPEIDWSAGVILYILLCGVPPFWAETEGQVAAILRGVLDPKRDPWPNVSNKDLV 297

Qy 247 KQMLEPDSYKRLTAQVLDHPWIONAKK 274
Db 298 RHMLEPDPKRLTAKQVLEHHWLQNAKK 325

RESULT 11
US-10-425-114-65930
; Sequence 65930, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 65930
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3606-058-A10_FLI.pep
; US-10-425-114-65930

Query Match      80.1%; Score 1136; DB 15; Length 592;
Best Local Similarity 79.1%; Pred. No. 6.2e-85;
Matches 212; Conservative 26; Mismatches 30; Indels 0; Gaps 0;

Qy 7 ISDKYILGRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 66
Db 113 IDDKYVLDRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 172

Qy 67 PEHPNVVKLKATYEDNETVHLMELCEGGELFGRIVARGHYTERAAATVARTIAEVVRMC 126
Db 173 PKSPSVVSLREACDDGAVHLVMECEGGELFGRIVARGHYTERAAASVTRTILEVVOLC 232

Qy 127 HVGVMHRDLKPENFLFANKKENSALKADIFGLSVLPKPGERFTEIVGSPYYMAPEVLKR 186
Db 233 HRHGVHHRDLKPENFLFANKKENSPLKADIFGLSIFPKGKEKFEIVGSPYYMAPEVLKR 292

Qy 187 NYGPEVDVMSAGVILYILLCGVPPFWAETEGQVALAILRGVLDPKRDPWQSOISSAKSLV 246
Db 293 NYGPEIDWSAGVILYILLCGVPPFWAETEGQVAAILRGVLDPKRDPWPNVSNKDLV 352

Qy 247 KQMLEPDSYKRLTAQVLDHPWIONAKK 274
Db 353 RHMLEPDPKRLTAKQVLEHHWLQNAKK 380

RESULT 13
US-10-767-701-44784
; Sequence 44784, Application US/10767701
; Publication No. US20040172684A1
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Db 113 IDDKYVLDRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 172
Qy 67 PEHPNVVKLKATYEDNETVHLMELCEGGELFGRIVARGHYTERAAATVARTIAEVVRMC 126
Db 173 PKSPSVVSLREACDDGAVHLVMECEGGELFGRIVARGHYTERAAASVTRTILEVVOLC 232
Qy 127 HVGVMHRDLKPENFLFANKKENSALKADIFGLSVLPKPGERFTEIVGSPYYMAPEVLKR 186
Db 233 HRHGVHHRDLKPENFLFANKKENSPLKADIFGLSIFPKGKEKFEIVGSPYYMAPEVLKR 292
Qy 187 NYGPEVDVMSAGVILYILLCGVPPFWAETEGQVALAILRGVLDPKRDPWQSOISSAKSLV 246
Db 293 NYGPEIDWSAGVILYILLCGVPPFWAETEGQVAAILRGVLDPKRDPWPNVSNKDLV 352
Qy 247 KQMLEPDSYKRLTAQVLDHPWIONAKK 274
Db 353 RHMLEPDPKRLTAKQVLEHHWLQNAKK 380

RESULT 12
US-10-425-114-70054
; Sequence 70054, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70054
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMOL1719A04_FLI.pep
; US-10-425-114-70054

Query Match      80.1%; Score 1136; DB 15; Length 592;
Best Local Similarity 79.1%; Pred. No. 6.2e-85;
Matches 212; Conservative 26; Mismatches 30; Indels 0; Gaps 0;

Qy 7 ISDKYILGRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 66
Db 113 IDDKYVLDRELGRGEGFITYLCTDRETREALACKSISKRLRTAVDVEDVRREVTIMSTL 172

Qy 67 PEHPNVVKLKATYEDNETVHLMELCEGGELFGRIVARGHYTERAAATVARTIAEVVRMC 126
Db 173 PKSPSVVSLREACDDGAVHLVMECEGGELFGRIVARGHYTERAAASVTRTILEVVOLC 232

Qy 127 HVGVMHRDLKPENFLFANKKENSALKADIFGLSVLPKPGERFTEIVGSPYYMAPEVLKR 186
Db 233 HRHGVHHRDLKPENFLFANKKENSPLKADIFGLSIFPKGKEKFEIVGSPYYMAPEVLKR 292

Qy 187 NYGPEVDVMSAGVILYILLCGVPPFWAETEGQVALAILRGVLDPKRDPWQSOISSAKSLV 246
Db 293 NYGPEIDWSAGVILYILLCGVPPFWAETEGQVAAILRGVLDPKRDPWPNVSNKDLV 352
Qy 247 KQMLEPDSYKRLTAQVLDHPWIONAKK 274
Db 353 RHMLEPDPKRLTAKQVLEHHWLQNAKK 380

RESULT 13
US-10-767-701-44784
; Sequence 44784, Application US/10767701
; Publication No. US20040172684A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44784
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C5983_1.pep
US-10-767-701-44784

Query Match      80.0%; Score 1135; DB 16; Length 425;
Best Local Similarity 78.7%; Pred. No. 5.1e-85;
Matches 21; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 7 ISDKYILGRELGRGFGITYLCTDRETREALACKSISKRLRTAVDVEDVRREVIMSTL 66
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 67 IDDKYALDRELGRGFGVTYLCMDRDTKELLACKSISKRLRTAVDVEDVRREVALMRHL 126
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 PEHPNVVCLKATYEDNETVHLVMECEGGEFGRIVARGHYTERAAATVARTIAEVVVMC 126
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 127 PKSPSIVSLREACEDEGAHVLVMECEGGEFGRIVARGHYTERAAANVTRTIVEVQVLC 192
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 127 HVGVMHRLDKPENFLFANKKENSALKAIIDFGLSVLPKGERFTEIVGSPYYMAPEVLKR 186
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 193 HRRGVTHRLDKPENFLFANKKENSPLKAIIDFGLSIFPKGEKFTSEIVGSPYYMAPEVLKR 252
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 187 NYGPEVDVMSAGVILYLLCGVPPFWAETEQGVALAILRGVLDPKRDPWSQISSEAKSLV 246
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 253 NYGPEIDVMSAGVILYLLCGVPPFWAETEQGVAQAILRGVLDPKRDPWPNVSENADLV 312
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 247 KQMLEPDPKRLTAQOVLDHPWQNAKK 274
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 313 RRMLEPDPKRLTAQOVLEHPWQNAKK 340
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-10-437-963-163957
; Sequence 163957, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 163957
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62904C.1.pep
US-10-437-963-163957

Query Match      78.6%; Score 1115; DB 16; Length 661;
Best Local Similarity 78.1%; Pred. No. 3.8e-83;
Matches 207; Conservative 27; Mismatches 31; Indels 0; Gaps 0;

QY 10 KYILGRELGRGFGITYLCTDRETREALACKSISKRLRTAVDVEDVRREVIMSTLPEH 69
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 63 RYELGELGRGFGITYLCTEATGDRYACKSISKRLRTAVDVEDVRREVEIMRHPMSH 122
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 70 PNVVCLKATYEDNETVHLVMECEGGEFGRIVARGHYTERAAATVARTIAEVVVMCHVN 129
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 123 PNIVSLRAAYEDEDNVHLVMECEGGEFGRIVARGHYTERAAATVARTIVEVQWCHRH 182
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 130 GVMHRLDKPENFLFANKKENSALKAIIDFGLSVLPKGERFTEIVGSPYYMAPEVLKRN 189
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 183 GVMHRLDKPENFLYANKKSSPLKAIIDFGLSVFFRGERFTEIVGSPYYMAPEVLKRYG 242
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 190 PEVDVMSAGVILYLLCGVPPFWAETEQGVALAILRGVLDPKRDPWSQISSEAKSLVKQM 249
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 243 PEVDVMSAGVILYLLCGVPPFWAETEQGVAQAILRSVVDPKREPWPVSEPAKDLVKRM 302
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 250 LEPDSTKRLTAQOVLDHPWQNAKK 274
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 303 LOPNPWTRLTABQVLEHPWLDHDSKK 327
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44784
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C5983_1.pep
US-10-767-701-44784

Query Match      80.0%; Score 1135; DB 16; Length 425;
Best Local Similarity 78.7%; Pred. No. 5.1e-85;
Matches 21; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 7 ISDKYILGRELGRGFGITYLCTDRETREALACKSISKRLRTAVDVEDVRREVIMSTL 66
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 67 IDDKYALDRELGRGFGVTYLCMDRDTKELLACKSISKRLRTAVDVEDVRREVALMRHL 126
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 PEHPNVVCLKATYEDNETVHLVMECEGGEFGRIVARGHYTERAAATVARTIAEVVVMC 126
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 127 PKSPSIVSLREACEDEGAHVLVMECEGGEFGRIVARGHYTERAAANVTRTIVEVQVLC 192
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 127 HVGVMHRLDKPENFLFANKKENSALKAIIDFGLSVLPKGERFTEIVGSPYYMAPEVLKR 186
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 193 HRRGVTHRLDKPENFLFANKKENSPLKAIIDFGLSIFPKGEKFTSEIVGSPYYMAPEVLKR 252
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 187 NYGPEVDVMSAGVILYLLCGVPPFWAETEQGVALAILRGVLDPKRDPWSQISSEAKSLV 246
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 253 NYGPEIDVMSAGVILYLLCGVPPFWAETEQGVAQAILRGVLDPKRDPWPNVSENADLV 312
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 247 KQMLEPDPKRLTAQOVLDHPWQNAKK 274
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 307 RRMLEPDPKRLTAQOVLEHHLWQNAKK 334
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-10-437-963-160820
; Sequence 160820, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 160820
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_60062C.1.pep
US-10-437-963-160820

Query Match      79.8%; Score 1132; DB 16; Length 599;
Best Local Similarity 78.7%; Pred. No. 1.3e-84;
Matches 21; Conservative 25; Mismatches 32; Indels 0; Gaps 0;
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Search completed: October 14, 2005, 11:02:47
Job time : 167 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2005, 10:58:37 ; Search time 40 Seconds

(without alignments)
659,085 Million cell updates/sec

Title: US-08-989-881-2

Perfect score: 1419

Sequence: 1 MANQTQISDKYILGRELGRG.....TKRLTAQQVLDHPWIONAKK 274

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1395	98.3	541	2	F96776	hypothetical prote
2	1322	93.2	545	2	H86322	calcium-dependent
3	1318	92.9	493	1	S46283	calcium-dependent
4	1161	81.8	560	2	T46189	calcium-dependent
5	1135	80.0	503	2	T51156	calcium-dependent
6	1127	79.4	530	2	A84847	probable Ca2+ depe
7	1127	79.4	533	1	S71778	calcium-dependent
8	1030	72.6	582	2	E84721	probable calcium-d
9	926	65.3	639	1	T02784	calcium-dependent
10	916	64.6	610	1	A49082	calcium-dependent
11	906	63.8	554	1	T03263	calcium-dependent
12	905.5	63.8	451	2	S56717	calcium-dependent
13	899	63.4	573	2	T09940	calcium-dependent
14	898	63.3	492	1	T03271	calcium-dependent
15	894.5	63.0	490	1	S71776	calcium-dependent
16	894	63.0	487	1	S71770	calcium-dependent
17	893	62.9	533	1	S56652	calcium-dependent
18	887	62.5	495	1	S46284	calcium-dependent
19	887	62.5	529	1	S71774	calcium-dependent
20	887	62.5	531	1	T02993	calcium-dependent
21	877.5	61.8	553	1	T02139	calcium-dependent
22	877	61.8	583	2	H84810	probable calcium-d
23	876	61.7	544	2	D84550	probable calmoduli
24	875	61.7	520	2	C84774	probable calcium-d
25	874	61.6	556	2	T06126	calcium-dependent
26	872	61.5	542	1	S56651	calcium-dependent
27	871	61.4	465	1	T03024	calcium-dependent
28	871	61.4	514	2	T10938	calcium-dependent
29	867	61.1	531	2	D85059	probable calcium d

30	866	61.0	520	2	F85059	probable calcium d
31	866	61.0	538	2	T08874	calcium-dependent
32	865	61.0	501	2	G85097	hypothetical prote
33	864	60.9	513	1	T02259	calcium-dependent
34	863	60.8	540	1	T01989	calcium-dependent
35	862	60.7	521	2	G96543	calcium-dependent
36	861.5	60.7	508	1	A43713	calcium-dependent
37	861	60.7	532	2	T14335	protein kinase, ca
38	857	60.4	490	2	T08873	calcium-dependent
39	854	60.2	484	2	T05650	calcium-dependent
40	850	59.9	554	2	T05476	calcium-dependent
41	822	57.9	534	1	JC1515	calcium-dependent
42	777	54.8	425	2	S17759	protein kinase, ca
43	744	52.4	571	2	T00835	calcium-dependent
44	737	51.9	591	2	S54788	calcium-stimulated
45	709	50.0	601	2	T46084	CDPK-related prote

ALIGNMENTS

RESULT 1

F96776

hypothetical protein F25A4.29 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: F96776

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marzai
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:1130712

A:Accession: F96776

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-541 <STO>

A:Cross-references: UNIPROT:Q9SSF8; GB:AE005173; NID:G5882721; PIDN:AAD55274.1; GSPDB:

C:Genetics:

A:Gene: F25A4.29

A:Map position: 1

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein k

C:Keywords: EF hand

Query Match 98.3%; Score 1395; DB 2; Length 541;
Best Local Similarity 98.2%; Pred. No. 4.8e-61; Mismatches 2; Indels 0; Gaps 0;
Matches 269; Conservative 3;

QY	1	MANQTQISDKYILGRELGRGFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREV	60
DB	49	MSHQSQISDKYILGRELGRGFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREV	108
QY	61	TIMSTLPHPNVKLVKATYEDNETVHLVNLCEGELFGRIVARGHYTERAAATVARTTA	120
DB	109	TIMSTLPHPNVKLVKATYEDNETVHLVNLCEGELFGRIVARGHYTERAAATVARTTA	168
QY	121	EVVRMCHVGMHRLKPELNFANKKNSALKALDFGLSVLFKPGERFTEVGSPPYMA	180
DB	169	EVVRMCHVGMHRLKPELNFANKKNSALKALDFGLSVLFKPGERFTEVGSPPYMA	228
QY	181	PEVLKRNYPGVDMVSAGVILYLLCGVPPFAETEQQGVALAILRGVLDFFKDPSPQISE	240
DB	229	PEVLKRNYPGVDMVSAGVILYLLCGVPPFAETEQQGVALAILRGVLDFFKDPSPQISE	288
QY	241	SAKSLVKOMLEPDSSTKRLTAQQVLDHPWIONAKK	274
DB	289	SAKSLVKOMLEPDSSTKRLTAQQVLDHPWIONAKK	322

RESULT 2
H86322
calcium-dependent protein kinase 1 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86322
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86322
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-545 <STO>
A;Cross-references: UNIPROT:Q9M9V8; GB:AE005172; NID:g6730697; PIDN:AAF27092.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C;Keywords: EF hand

Query Match 93.2%; Score 1322; DB 2; Length 545;
Best Local Similarity 92.3%; Pred. No. 1.6e-57;
Matches 253; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
Qy 1 MANQTQISDKYILGRELGRGFGITLYCTDRETHALACKSISKRKLRTAVDVEDVRREV 60
Db 53 MSNQTQISDKYILGRELGRGFGITLYCTDRETHALACKSISKRKLRTAVDIEDVRREV 112
Qy 61 TIMSTLPEHPNVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAAVARTIA 120
Db 113 AIMSTLPEHPNVVKLKASYEDNENVHLMELCEGELFDRIVARGHYTERAAAAVARTIA 172
Qy 121 EVVRMCHVNGVMHRLDKPENFLFANKKENSALKADFGSLVLPKPGGRFTEIVGSPYMA 180
Db 173 EVVMCHSNGVMHRLDKPENFLFANKKENSPLKADFGSLVFPKPGDKFTEIVGSPYMA 232
Qy 181 PEVLKRNYPGEVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISE 240
Db 233 PEVLKRDYGPVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISE 292
Qy 241 SAKSLVKQMLPDPSTKRLTAQOVLDPHPIQNAKK 274
Db 293 SAKSLVKQMLPDPSTKRLTAQOVLDPHPIQNAKK 326

RESULT 3
S46283
calcium-dependent protein kinase (EC 2.7.1.1) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: S46283
R;Urao, T.; Katagiri, T.; Mizoguchi, T.; Yamaguchi-Shinozaki, K.; Hayaashida, N.; Shinoza
Mol. Gen. Genet. 244, 331-340, 1994
A;Title: Two genes that encode Ca(2+)-dependent protein kinases are induced by drought a
A;Reference number: S46283; MUID:943359455; PMID:8078458
A;Accession: S46283
A;Molecule type: mRNA
A;Residues: 1-493 <URA>
A;Cross-references: UNIPROT:Q39015; EMBL:D21805; NID:g1235716; PIDN:BAA04829.1; PID:g604
C;Genetics:
A;Gene: CDPK1
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F;9-269/Domain: protein kinase homology <kin>
F;17-25/Region: protein kinase ATP-binding motif

F;312-344/Domain: calmodulin repeat homology <EF1>
F;348-380/Domain: calmodulin repeat homology <EF2>
F;384-416/Domain: calmodulin repeat homology <EF3>
F;420-452/Domain: calmodulin repeat homology <EF4>
F;40/Active site: Lys #status predicted

Query Match 92.9%; Score 1318; DB 1; Length 493;
Best Local Similarity 92.0%; Pred. No. 2.4e-57;
Matches 252; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
Qy 1 MANQTQISDKYILGRELGRGFGITLYCTDRETHALACKSISKRKLRTAVDVEDVRREV 60
Db 1 MSNQTQISDKYILGRELGRGFGITLYCTDRETHALACKSISKRKLRTAVDIEDVRREV 60
Qy 61 TIMSTLPEHPNVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAAVARTIA 120
Db 61 AIMSTLPEHPNVVKLKASYEDNENVHLMELCEGELFDRIVARGHYTERAAAAVARTIA 120
Qy 121 EVVRMCHVNGVMHRLDKPENFLFANKKENSALKADFGSLVLPKPGGRFTEIVGSPYMA 180
Db 121 EVVMCHSNGVMHRLDKPENFLFANKKENSPLKADFGSLVFPKPGDKFTEIVGSPYMA 180
Qy 181 PEVLKRNYPGEVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISE 240
Db 181 PEVLKRDYGPVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISE 240
Qy 241 SAKSLVKQMLPDPSTKRLTAQOVLDPHPIQNAKK 274
Db 241 SAKSLVKQMLPDPSTKRLTAQOVLDPHPIQNAKK 274

RESULT 4

T46189
calcium-dependent protein kinase - Arabidopsis thaliana
N;Alternate names: protein T8H10.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46189
R;Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, January 2000
A;Reference number: 223014
A;Accession: T46189
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-560 <BEN>
A;Cross-references: UNIPROT:Q9SCMO; EMBL:AL133248
A;Experimental source: cultivar Columbia; BAC clone T8H10
C;Genetics:
A;Map position: 3
A;Introns: 176/3; 218/1; 266/1; 317/1; 355/3; 411/3; 487/3; 532/3
A;Note: T8H10.130
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki
C;Keywords: EF hand

Query Match 81.8%; Score 1161; DB 2; Length 560;
Best Local Similarity 79.5%; Pred. No. 1.1e-49;
Matches 213; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

Qy 6 QISDKYILGRELGRGFGITLYCTDRETHALACKSISKRKLRTAVDVEDVRREVIMST 65
Db 58 EIESKYTLGRELGRGFGITLYCTDRETHALACKSISKRKLRTAVDIEDVRREVIMRH 117
Qy 66 LPEHPNVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAAVARTIAEVVRM 125
Db 118 MPEHPNVVTLKETYEDEHAVHLMELCEGELFDRIVARGHYTERAAAAVTIMEVQV 177
Qy 126 CHVNGVMHRLDKPENFLFANKKENSALKADFGSLVLPKPGGRFTEIVGSPYMAPEVLK 185
Db 178 CHKGVHRLDKPENFLFGNKETAFLKADFGSLVFPKPGDKFTEIVGSPYMAPEVLK 237
Qy 186 RNYGPEVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISEAKSL 245
Db 238 RNYGPEVDVWSAGVILYILLCGVPFPAETEQGVVALAILRGVLDKFRDWPQISEAKSL 297

Qy	7	ISDKVILGREIGREBFGITYILCTDRETBALACKSISKKRLTAVDVEDVREVTIMSTL	66
Db	53	ISLMYDLGREVGRBFGITYILCTDITKTGEKAYSISKKKRLTAVDIEDVREVEIMKHM	112
Qy	67	PEHENVKLKATYEDNETWHLVMEICEGELFGRIVARGHYTERAAATVARITAEVVMC	126
Db	113	PRHPNIVSLKDAFEDDDAVHVMELCEGELFDRIVARGHYTERAAAAVMKTIILEVQIC	172
Qy	127	HVNGVMHRDLKPENPLFANKKENSALKALDFGLSVLPKPGERFTEIVGSPYMAPEVLKR	186
Db	173	HKHGVMHRDLKPENFLFANKKETSALKALDFGLSVFFKPGEGFNIVGSPYMAPEVLKR	232
Qy	187	NYGPEVDVWSAGVILYILLCGVPPPWAETEOQVLAAILRLGVLDKFKDPWSQISESAKSIV	246
Db	233	NYGPEVDIWSAGVILYILLCGVPPPWAETEOQVAQAIIRSVLIDFKRDPWPVSETAKOLV	292
Qy	247	KQMLEPSTKRLTTAQVLDHPWIQNAKK	274
Db	293	KQMLEPDPKKRLSAAQVLEHSWIQNAKK	320

RESULT 8
E84721
probable calcium-dependent protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84721
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii,
M.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tal-
euss, D.; Nierman, W.C.; White, N.A.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ve-
nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84721
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-582 <STO>
A:Cross-references: UNIPROT:Q9SIQ7; GB:AE002093; NID:G4582467; PIDN:AAD24851.1; G
C:Genetics:
A:Gene: At2g31500
A:Map position: 2
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; prot
C:Keywords: EF hand

RESULT 9
T02784
calcium-dependent protein kinase (EC 2.7.1.-) - maize (strain W64A)
C:Species: Zea mays (maize)

C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C; Accession: T02784
R; Murillo, I.; Jaeck, E.; Cordero, M.; San Segundo, B.
submitted to the EMBL Data Library, July 1998
A; description: A calcium-dependent protein kinase possibly involved in patho-
sis-related PRMs gene.
A; Reference number: Z14736
A; Accession: T02784
A; Status: translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-639 <MUR>
A; Cross-references: UNIPROT:O82107; EMBL-AJ007366; PIDN:CAA07481.1
A; Experimental source: strain W64A; seed

RESULT 10
A49082
calcium-dependent protein kinase (EC 2.7.1.-) AK1 - Arabidopsis thaliana
C Species: Arabidopsis thaliana (mouse-ear cress)
C Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
R Accession: A49082
R Harper, J.F.; Binder, B.M.; Sussman, M.R.
Biochemistry 32, 3282-3290, 1993
A Title: Calcium and lipid regulation of an Arabidopsis protein kinase expressed in *Escherichia coli*
A Reference number: A49082; MUID:93213795; PMID:7916621

2

A:Gene: CPK1
 C:Function: serine/threonine-specific protein kinase activated by direct binding of calcium
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
 C:Keywords: ATP; calcium binding; EF hand; membrane protein; myristylation; phosphotransferase
 F:108-368/Domain: protein kinase homology <KIN>
 F:447-479/Domain: calmodulin repeat homology <EFH>

Query Match 63.4%; Score 899; DB 2; Length 573;
 Best Local Similarity 63.4%; Pred. No. 5.2e-37;
 Matches 168; Conservative 36; Mismatches 61; Indels 0; Gaps 0;

Qy 11 YILGRELGRGPIYTLCTDRETRALACKSISKRLTAVDVEDVREVTIMSTLPBHP 70
 Db 110 YSLGKLGQGGQGTTCVCKATKEYAKSLAKLVNEDDVEDVREIQTIMHLSGHP 169
 Qy 71 NVVKKATYEDNETVHLVNLCEGGEFGIIVARGHYTERAAATVARTIAEVVRCHVNG 130
 Db 170 NVISIKGAYEDAVAVQVWMLCAGGELPDRIIQRGHYTERKAAELTRIIVGVLEACHALG 229
 Qy 131 VMHRLDKPENFLFANKKENSALKADIFGLSVLFKPGERTFTEIVGSPYYMAPEVLKKNYGP 190
 Db 230 VMHRLDKPENFLFVSKESLKTIDFGLSMFKPGKFNVDVVGSPYYVAPEVLKRYGP 289
 Qy 191 EVDVMSAGVILYLLCGVPPFAETEQGVVALAILRGVLDPKEDPKSQISSESAKSLVKWL 250
 Db 290 EADVMSAGVIVYLLSGVPPFAESEGFEIVLHGLDLDFFSDPWPSPISDSAKDLVRRML 349
 Qy 251 EPDSTKRLTAQOVLDPHWIQ 270
 Db 350 VRDPRKRLTAIEVLCHPWVQ 369

RESULT 14

T03271
 calcium-dependent protein kinase (EC 2.7.1.1) 1 - maize
 C:Species: Zea mays (maize)
 C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
 C:Accession: T03271
 R:Berberich, T.; Kusano, T.
 Mol. Gen. Genet. 254, 275-283, 1996
 A:Title: Cycloheximide induces a subset of low temperature-inducible genes in maize.
 A:Reference number: Z14873
 A:Accession: T03271
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-492 <BER>
 A:Cross-references: UNIPROT:O04417; EMBL:D84408; PIDN:BAA12338.1
 A:Experimental source: strain honey bantum
 A:Note: low temperature-inducible
 C:Genetics:

A:Gene: CDPK1
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
 C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
 F:25-285/Domain: protein kinase homology <KIN>
 F:33-41/Region: protein kinase ATP-binding motif
 F:328-360/Domain: calmodulin repeat homology <EF1>
 F:364-396/Domain: calmodulin repeat homology <EF2>
 F:400-432/Domain: calmodulin repeat homology <EF3>
 F:434-466/Domain: calmodulin repeat homology <EF4>
 F:56/Active site: Lys #status predicted

Query Match 63.3%; Score 898; DB 1; Length 492;
 Best Local Similarity 63.4%; Pred. No. 5.2e-37;
 Matches 168; Conservative 36; Mismatches 61; Indels 0; Gaps 0;

Qy 7 ISDKYILGRELGRGFGITLCTDRETRALACKSISKRLTAVDVEDVREVTIMSTL 66
 Db 23 LRDLVALGRUGGGQGTITLCTELATGIDYACKSISKRLTKEDVDVREIQTIMHLL 82
 Qy 67 PPHNPVKKATYEONETVHLVNLCEGGEFGIIVARGHYTERAAATVARTIAEVVRMC 126
 Db 83 SGHKNVKAGAYEDQVYVHVLWELCAGGELPDRIIQRGHYTERKAAALTRIIVGVVEAC 142

Qy 127 HVGVMHRLDKPENFLFANKKENSALKADIFGLSVLFKPGERTFTEIVGSPYYMAPEVLKLR 186
 Db 143 HSLGVMHRLDKPENFLANRDDDUSLKAIDFGLSVFVKPGQVFTDVVGSPIYVAPEVLK 202
 Qy 187 NYGPEVDVMSAGVILYLLCGVPPFAETEQGVVALAILRGVLDPKEDPKSQISSESAKSLV 246
 Db 203 SYGPAADVWTAGVILYLLSGVPPFAETEQGIFDAVLKGAIDFSDPWPVSDSAKDLI 262
 Qy 247 KOMLEPSTKRLTAQOVLDPHWIQ 271
 Db 263 RRMLNPRPAERLTAHEVLCHPWIRD 287

RESULT 15

S71776
 calcium-dependent protein kinase (EC 2.7.1.1) 9 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
 C:Accession: S71776; S71775; S71902; S71196
 R:Hong, Y.; Takano, M.; Liu, C.M.; Gassch, A.; Chye, M.L.; Chua, N.H.
 Plant Mol. Biol. 30, 1259-1275, 1996
 A:Title: Expression of three members of the calcium-dependent protein kinase gene family
 A:Reference number: S71774; MUID:96311013; PMID:8704134

A:Accession: S71776
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-490 <HON>
 A:Cross-references: UNIPROT:Q42396; EMBL:U20626
 A:Accession: S71775
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-490 <HOP>

A:Cross-references: EMBL:U20388
 R:Hong, Y.; Takano, M.; Liu, C.M.; Gassch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N.
 submitted to the EMBL Data Library, February 1995
 A:Description: Expression of the calcium-dependent protein kinase gene family in Arabidopsis
 A:Reference number: S71197
 A:Accession: S71902
 A:Molecule type: DNA
 A:Residues: 1-164, 'S', 166-239, 'E', 241-300, 'KF', 303-350, 'S', 352-490 <HOW>
 A:Cross-references: EMBL:U20626; NID:9836945; PIDN:AAA67657.1; PID:9836946
 R:Hong, Y.; Takano, M.; Liu, C.M.; Gassch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N.
 submitted to the EMBL Data Library, January 1995

A:Description: Expression of the calcium dependent protein kinase gene family in Arabidopsis
 A:Reference number: S71196
 A:Accession: S71196
 A:Molecule type: mRNA
 A:Residues: 1-164, 'S', 166-239, 'E', 241-300, 'KF', 303-350, 'S', 352-490 <HOA>
 A:Cross-references: EMBL:U20388; NID:9836937; PIDN:AAA67653.1; PID:9836938
 C:Genetics:

A:Gene: CDPK9
 A:Introns: 177/1; 225/1; 276/1; 370/3; 445/3
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
 C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
 F:20-280/Domain: protein kinase homology <KIN>
 F:28-36/Region: protein kinase ATP-binding motif
 F:323-355/Domain: calmodulin repeat homology <EF1>
 F:359-391/Domain: calmodulin repeat homology <EF2>
 F:395-427/Domain: calmodulin repeat homology <EF3>
 F:429-461/Domain: calmodulin repeat homology <EF4>
 F:51/Active site: Lys #status predicted

Query Match 63.0%; Score 894.5; DB 1; Length 490;
 Best Local Similarity 60.2%; Pred. No. 7.6e-37;
 Matches 171; Conservative 41; Mismatches 61; Indels 11; Gaps 1;

Qy 1 MANOTQ-----ISDKYILGRELGRGFGITLCTDRETRALACKSISKRLKRT 49
 Db 1 MANPRTRWLPYTKKVEDNYFLGVGGQGGTTFLCTHKQTGQKLACKSIPKRLJC 60
 Qy 50 ADVVEDVRREVTIMSTLPEHPNVKLYKATYEDNETVHLVNLCEGGEFGIIVARGHYTERAAALTRIIVGVVEAC 109

```

Db      61 QEDYDDVLRRIQIMHHLSEYPNVVRIESAYEDTKNVHVMELCEGGELFDRIVKRGHYSE 120
Qy      110 RAAATVARTIAEVVRMCHVGMHRDLKPENFLPANKKENSALKAIIDFGLSVLFKPCGERF 169
Db      121 REAAKLIKTIIVGVVEACHSLGVVHRDLKPENFLFSSSDEDEASLKATDFGLSVFCTPGEAF 180
Qy      170 TEIVGSPYNAPEVLKKNYGPEDVMSAGVILYLLCGVPPFWAETEOGVVALAILRGVLD 229
Db      181 SELVGSAYYVAPEVLHKHYGPECVMSAGVILYLLCGFPFFWAESIEIGIFRKILQKLD 240
Qy      230 FKRDPMWSQISESAKSLVKOMLEPDSTKRLTAQQVLDHPWIONAK 273
Db      241 FEINPMPSISESAKDLIKKMLESNPKKRLTAHQVLCHPWIVDDK 284

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Search completed: October 14, 2005, 11:09:27
 Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2005, 10:54:56 ; Search time 176 Seconds
(without alignments)
797.214 Million cell updates/sec

Title: US-08-989-881-2
Perfect score: 1419
Sequence: 1 MANQTOISDKVILGRELGRG.....TKRLTAQVLDHPWQNAKK 274

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	1419	100.0	274	Q9SB23	Q9sb23 arabidopsis
2	1395	98.3	541	Q9SPF8	Q9sf8 arabidopsis
3	1322	93.2	545	Q9M9V8	Q9m9v8 arabidopsis
4	1318	92.9	493	Q3Q015	Q3q015 arabidopsis
5	1318	92.9	545	Q84W07	Q84w07 arabidopsis
6	1186	83.6	518	Q94G52	Q94g52 funaria hyg
7	1161	81.8	538	Q6NLQ6	Q6nlq6 arabidopsis
8	1161	81.8	560	Q9SCM0	Q9scm0 arabidopsis
9	1158	81.6	529	Q48565	Q48565 fragaria an
10	1155	81.4	550	Q84SL0	Q84sl0 oryza sativ
11	1142	80.5	528	Q6KC54	Q6kc54 nicotiana p
12	1141	80.4	522	Q8HIT8	Q8hit8 ceratopteris
13	1141	80.4	535	Q38873	Q38873 arabidopsis
14	1135	80.0	503	Q96294	Q96294 arabidopsis
15	1135	80.0	528	Q8W4I7	Q8w4i7 arabidopsis
16	1132	79.8	551	Q8LKE27	Q8lke27 oryza sativ
17	1127	79.4	530	Q93759	Q93759 arabidopsis
18	1127	79.4	533	Q42438	Q42438 arabidopsis
19	1115	78.6	538	Q75G88	Q75g88 oryza sativ
20	1106	77.9	547	Q6I5I8	Q6i5i8 oryza sativ
21	1094	77.1	574	Q6AVI8	Q6avi8 oryza sativ
22	1030	72.6	582	Q8G3T5	Q8g3t5 arabidopsis
23	1030	72.6	582	Q9SIQ7	Q9siq7 arabidopsis
24	957	67.4	548	Q9S786	Q9s786 marchantia
25	957	67.4	548	Q9S724	Q9s724 marchantia
26	932	65.7	599	Q6F3A6	Q6f3a6 oryza sativ
27	930	65.5	528	Q8VYE7	Q8vye7 arabidopsis
28	929.5	65.5	577	Q69IM9	Q69im9 oryza sativ
29	929	65.5	528	Q9FWP5	Q9fwp5 arabidopsis
30	926	63.9	639	Q82107	Q82107 zea mays (m
31	919	64.8	646	Q38870	Q38870 arabidopsis

RESULT 1

ID	Q9SB23	PRELIMINARY;	PRT;	274 AA.
AC	Q9SB23;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	AtCDPK1a (Fragment).			
GN	Name=cpk1a;			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Sheen J.;			
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
DR	EMBL; U73610; AAF14337.1; -.			
DR	HSSP; P49137; INXK.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0016740; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0006468; F:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR011009; Kinase_like.			
DR	InterPro; IPR00719; Prot_kinase.			
DR	InterPro; IPR002290; Ser_thr_pkinase.			
DR	InterPro; IPR008271; Ser_thr_pkin_AS.			
DR	Pfam; PF00069; Pkinase_I.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00220; S_TKc; 1.			
DR	PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.			
DR	PROSITE; PS00111; PROTEIN KINASE DOM; 1.			
DR	PROSITE; PS00108; PROTEIN KINASE ST; 1.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
FT	NON_TER 274 274			
SQ	SEQUENCE 274 AA; 30909 MW; 8C6E5A1B0972265D CRC64;			

Query Match 100.0%; Score 1419; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 2.2e-89;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MANQTOISDKVILGRELGRGFGITVLTCDRETREALACKSISKRLRTAVDVEDVREV	60
Db	1	MANQTOISDKVILGRELGRGFGITVLTCDRETREALACKSISKRLRTAVDVEDVREV	60
Qy	61	TTMSTLPEHPNVVVKLKYEDNETVHLVNLCEGGLFGRIVARGHYTERAAATVARTIA	120
Db	61	TTMSTLPEHPNVVVKLKYEDNETVHLVNLCEGGLFGRIVARGHYTERAAATVARTIA	120
Qy	121	EYVRMCHVNGVMHRLDKPENFLFANKKENSALKAFIDGLSVLPFKGERFTEIVGSPYYMA	180
Db	121	EYVRMCHVNGVMHRLDKPENFLFANKKENSALKAFIDGLSVLPFKGERFTEIVGSPYYMA	180

QY 181 PEVLKRNYPGVDSAGVILYLLCGVPPFWAETQGVVALAILRGVLDKRDPSQISE 240
 |||||
 DB 181 PEVLKRNYPGVDSAGVILYLLCGVPPFWAETQGVVALAILRGVLDKRDPSQISE 240
 |||||
 QY 241 SAKSLVKQMLEPDSKRLTAQOVLDPHPWQNAKK 274
 |||||
 DB 241 SAKSLVKQMLEPDSKRLTAQOVLDPHPWQNAKK 274
 |||||

RESULT 2
 Q9S8F8 PRELIMINARY; PRT; 541 AA.

AC Q9S8F8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE F25A4.29 protein (Atlg74740) (Calcium-dependent protein kinase,
 putative).
 GN Name=F25A4.29; Synonyms=Atlg74740;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
 RA Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,
 RA Chin C., Choi E., Chiou J., Alrafi H., Araujo R., Brooks S.,
 RA Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
 RA Hwang B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
 RA Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
 RA Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.,
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AC008263; AAD55274.1; -;
 DR EMBL; BT008900; AAP68339.1; -;
 DR EMBL; AY140016; AM98158.1; -;
 DR PIR; F96776; F96776.
 DR HSP; P49137; INXX.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR010983; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00054; EFh; 4.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS0018; EF HAND; UNKNOWN 4.
 DR PROSITE; PS0107; PROTEIN KINASE ATP; UNKNOWN 1.
 DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 541 AA; 61404 MW; 7D170F76BAFCB4C4 CRC64;

Query Match 98.3%; Score 1395; DB 2; Length 541;
 Best Local Similarity 98.2%; Pred. No. 2e-87;
 Matches 269; Conservative 3; Mismatches 0; Gaps 0;

QY 1 MANQTQISDKVILGRELGRGFGITYLCTDRETREALACKSISKRLRTAVDVEVRREV 60
 |||||
 DB 49 MSHQSQISDKVILGRELGRGFGITYLCTDRETREALACKSISKRLRTAVDVEVRREV 108
 |||||
 QY 61 TIMSTLPEHPNVKATYEDNEVHLVMECEGELFGRIVARGHYTERAAATVARTIA 120
 |||||
 DB 109 TIMSTLPEHPNVKATYEDNEVHLVMECEGELFGRIVARGHYTERAAATVARTIA 168
 |||||
 QY 121 EVVRMCHVNGVYHRDLKPEFLFANKKENSALKALDFGLSVLFKPGERFTEIVGSPYMA 180
 |||||
 DB 169 EVVRMCHVNGVYHRDLKPEFLFANKKENSALKALDFGLSVLFKPGERFTEIVGSPYMA 228
 |||||
 QY 181 PEVLKRNYPGVDSAGVILYLLCGVPPFWAETQGVVALAILRGVLDKRDPSQISE 240
 |||||
 DB 229 PEVLKRNYPGVDSAGVILYLLCGVPPFWAETQGVVALAILRGVLDKRDPSQISE 288
 |||||
 QY 241 SAKSLVKQMLEPDSKRLTAQOVLDPHPWQNAKK 274
 |||||
 DB 289 SAKSLVKQMLEPDSKRLTAQOVLDPHPWQNAKK 322
 |||||

RESULT 3
 Q9M9V8 PRELIMINARY; PRT; 545 AA.

ID Q9M9V8;
 AC Q9M9V8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Calcium-dependent protein kinase 1.
 GN Name=FA14.1;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
 RA Lucos S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.,
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AC011809; AAF27092.1; -;
 DR PIR; H86322; H86322.
 DR HSP; P49137; INXX.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR02048; EF-hand.
 DR InterPro; IPR010983; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkin_AS.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00020; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 545 AA; 61459 MW; A505FB320E7818E9 CRC64;

Query Match 93.2%; Score 1322; DB 2; Length 545;
Best Local Similarity 92.3%; Pred. No. 2e-82;
Matches 253; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 MANQTQISDKYILGRELGRGEFGITVLTCDRETRALACKSISKRKLRTAVDVEDVREV 60
DB 53 MSNQTQISDKYILGRELGRGEFGITVLTCDRETRALACKSISKRKLRTAVDIEDVREV 112
QY 61 TIMSTLPEHPNVVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIA 120
DB 113 AINSTLPEHPNVVVKLKASYEDNENHLMELCEGELFDRIVARGHYTERAAAVARTIA 172
QY 121 EYVMCHVNGVWHRDLKPENFLFANKKENSALKALDAFGLSVLPKPGERFTEIVGSPYMA 180
DB 173 EYVMCHSNGVWHRDLKPENFLFANKKENSPLKALDAFGLSVFPKPGDKFTEIVGSPYMA 232
QY 181 PEVLKKNYGEVDVWSAGVILYLLCGVPPFWAETEGQVALAILRGVLDKRPDPWPOISE 240
DB 233 PEVLKRDYGFVDVWSAGVILYLLCGVPPFWAETEGQVALAILRGVLDKRPDPWPOISE 292
QY 241 SAKSLVKQMLEPDPSTKRLTAQVLDHPWIONAKK 274
DB 293 SAKSLVKQMLDPTKRLTAQVLAHPWIONAKK 326

RESULT 4
Q39015 PRELIMINARY; PRT; 493 AA.

ID Q39015
AC Q39015
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calcium-dependent protein kinase.
GN Name-ATCDPK1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
[1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=94359455; PubMed=8078458;
RA Urao T., Katagiri T., Mizoguchi T., Yamaguchi-Shinozaki K.,
RA Hayashida N., Shinozaki K.;
RT "Two genes that encode Ca2+-dependent protein kinases are induced by
drought and high-salt stresses in Arabidopsis thaliana.";
RL Mol. Gen. Genet. 244:331-340(1994).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; D21805; BAA04823.1; -;
DR PIR; S46283; S46283.
DR HSP; P49137; INXK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF-hand.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR Pfam; PF000036; efhand; 4.
DR Pfam; PF000029; Pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00020; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 493 AA; 55685 MW; 6B62B49BD17D3C12 CRC64;

Query Match 92.9%; Score 1318; DB 2; Length 493;
Best Local Similarity 92.0%; Pred. No. 3.4e-82;
Matches 252; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MANQTQISDKYILGRELGRGEFGITVLTCDRETRALACKSISKRKLRTAVDVEDVREV 60
DB 53 MSNQTQISDKYILGRELGRGEFGITVLTCDRETRALACKSISKRKLRTAVDIEDVREV 60
QY 61 TIMSTLPEHPNVVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIA 120
DB 113 AINSTLPEHPNVVVKLKASYEDNENHLMELCEGELFDRIVARGHYTERAAAVARTIA 120
QY 121 EYVMCHVNGVWHRDLKPENFLFANKKENSALKALDAFGLSVLPKPGERFTEIVGSPYMA 180
DB 173 EYVMCHSNGVWHRDLKPENFLFANKKENSPLKALDAFGLSVFPKPGDKFTEIVGSPYMA 180
QY 181 PEVLKKNYGEVDVWSAGVILYLLCGVPPFWAETEGQVALAILRGVLDKRPDPWPOISE 240
DB 233 PEVLKRDYGFVDVWSAGVILYLLCGVPPFWAETEGQVALAILRGVLDKRPDPWPOISE 240
QY 241 SAKSLVKQMLEPDPSTKRLTAQVLDHPWIONAKK 274
DB 293 SAKSLVKQMLDPTKRLTAQVLAHPWIONAKK 274

RESULT 5
Q84W07 PRELIMINARY; PRT; 545 AA.

ID Q84W07
AC Q84W07
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE At1g18890.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
[1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=94359455; PubMed=8078458;
RA Urao T., Katagiri T., Mizoguchi T., Yamaguchi-Shinozaki K.,
RA Hayashida N., Shinozaki K.;
RT "Two genes that encode Ca2+-dependent protein kinases are induced by
drought and high-salt stresses in Arabidopsis thaliana.";
RL Mol. Gen. Genet. 244:331-340(1994).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; D21805; BAA04823.1; -;
DR PIR; S46283; S46283.
DR HSP; P49137; INXK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF-hand.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.

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DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 545 AA; 61487 MW; 6957D76A1E7D93E4 CRC64;

Query Match      92.9%; Score 1318; DB 2; Length 545;
Best Local Similarity 92.0%; Pred. No. 3.8e-82;
Matches 252; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MANQTOISDKYLGRGLGRGFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREV 60
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
53 MSNQTQISDKYLGRGLGRGFGITYLCTDRETRALACKSISKRLRTAVDIEDVRREV 112
QY 61 TIMSTLPEHPNVVVKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIA 120
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 AIMSTLPEHPNVVVKASYEDNENVHLMELCEGELFDRIVARGHYTERAAAAVVRTIA 172
QY 121 EYVRCHVNGVMHRDLKPNFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYMA 180
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
173 EVVMCHSNGVMHRDLKPNFLFANKKENSPLKKAIDFGLSVFPKGERFTEIVGSPYYMA 232
QY 181 PEVLKRNYPGVVDVMSAGVILYLLCGVPPFPAETEGQVALAILRGVLDFKRDPMQISE 240
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
233 PEVLKRDYGPVVDVMSAGVILYLLCGVPPFPAETEGQVALAILRGVLDFKRDPMQISE 292
QY 241 SAKSLVKOMLEPDSSTKRLTAQOVLDPHPIQNAKK 274
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
293 SAKSLVKOMLEPDPKRLTAQOVLDPHPIQNAKK 326

RESULT 6
Q94G52 PRELIMINARY; PRT; 518 AA.
AC Q94G52;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calcium-dependent protein kinase (Fragment).
OS Funaria hygrometrica (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Funaria.
OX NCBI_TaxID=29583;
RN [1]
RP SEQUENCE FROM N.A.
RA Mitra D., Johri M.M.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AA62812.1; -
DR HSSP; P49137; 1NXX.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkin_AS.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.

DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 518 AA; 58817 MW; 344046C5D6E847B8 CRC64;

Query Match      83.6%; Score 1186; DB 2; Length 518;
Best Local Similarity 81.9%; Pred. No. 3.9e-73;
Matches 222; Conservative 18; Mismatches 31; Indels 0; Gaps 0;

QY 4 QTOISDKYLGRGLGRGFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREV 63
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33 KARILDKYVLGRGLGRGFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREV 92
QY 64 STLPEHPNVVVKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIAEV 123
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
93 KHLPEHPNVVTKGAYEDDNVHLMELCEGELFDRIVARGHYTERGAAQVTRTIVEV 152
QY 124 RMCHVNGVMHRDLKPNFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYMAPEV 183
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
153 QACHRQGMHRDLKPNFLFANKKENSPLKKAIDFGLSVFPKGERFTEIVGSPYYMAPEV 212
QY 184 LKRNYPGVVDVMSAGVILYLLCGVPPFPAETEGQVALAILRGVLDFKRDPMQISESAK 243
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
213 LKRNYPGVVDVMSAGVILYLLCGVPPFPAETEGQVALAILRGVLDFKRDPMQISESAK 272
QY 244 SLVKOMLEPDSSTKRLTAQOVLDPHPIQNAKK 274
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
273 SLVRHMLEPDPKARYIAQQVLDHPWLQNAKK 303

RESULT 7
Q6NLQ6 PRELIMINARY; PRT; 538 AA.
AC Q6NLQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AC3957530.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BT012274; AAS76761.1; -
DR EMBL; BT011630; AAS47636.1; -
DR HSSP; O63450; 1A06.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR010983; EF_Hand_like.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkin_AS.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
```

DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 538 AA; 60935 MW; FAD0C733CB85C810 CRC64;

Query Match 81.8%; Score 1161; DB 2; Length 538;
Best Local Similarity 79.5%; Pred. No. 2.1e-71;
Matches 213; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

QY 6 QISDKYILGRLGGEFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREVIMST 65
DB 58 EIESKYTLGRLGGEFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREVIMRH 117
QY 66 LPEHPNVVVKATYEDNETVHLVLMELCEGGEFGIRIVARGHYTERAAATVARTIAEVVRM 125
DB 118 MPEHPNVVTKETYEDEHAVHLVLMELCEGGEFGIRIVARGHYTERAAATVKTIVVQV 177
QY 126 CHVNGVWHRDLKPNFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYNAPEVLK 185
DB 178 CHKGVWHRDLKPNFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYNAPEVLK 237
QY 186 RNYGPEVDVMSAGVILYLLCGVPPFWAETEQGVALAILRGVLDPKRDPKSOISEAKSL 245
DB 238 RNYGPEVDVMSAGVILYLLCGVPPFWAETEQGVALAILRGVLDPKRDPKSOISEAKSL 297

RESULT 8
Q9SCM0 PRELIMINARY; PRT; 560 AA.
AC Q9SCM0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calcium-dependent protein kinase.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AL133248; CAB86110.1; -;
DR PIR; T46189; T46189.
DR HSSP; P49137; INXK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006468; P:proteinase activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR010983; EF Hand like.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 560 AA; 63409 MW; 4691E7A7D14B1CDO CRC64;

Query Match 81.8%; Score 1161; DB 2; Length 560;
Best Local Similarity 79.5%; Pred. No. 2.2e-71;
Matches 213; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

QY 6 QISDKYILGRLGGEFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREVIMST 65
DB 58 EIESKYTLGRLGGEFGITYLCTDRETRALACKSISKRLRTAVDVEDVRREVIMRH 117
QY 66 LPEHPNVVVKATYEDNETVHLVLMELCEGGEFGIRIVARGHYTERAAATVARTIAEVVRM 125
DB 118 MPEHPNVVTKETYEDEHAVHLVLMELCEGGEFGIRIVARGHYTERAAATVKTIVVQV 177
QY 126 CHVNGVWHRDLKPNFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYNAPEVLK 185
DB 178 CHKGVWHRDLKPNFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYNAPEVLK 237
QY 186 RNYGPEVDVMSAGVILYLLCGVPPFWAETEQGVALAILRGVLDPKRDPKSOISEAKSL 245
DB 238 RNYGPEVDVMSAGVILYLLCGVPPFWAETEQGVALAILRGVLDPKRDPKSOISEAKSL 297

RESULT 9
Q48565 PRELIMINARY; PRT; 529 AA.
AC Q48565;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calcium-dependent protein kinase.
GN Names=MAX17;
OS Fragaria ananassa (Strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=3747;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fruit;
RA Llop-Tous I., Dominguez-Puigjaner E., Vendrell M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF035944; AAB88537.1; -;
DR HSSP; P49137; INXK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006468; P:proteinase activity; IEA.
DR InterPro; IPR010983; EF Hand like.
DR InterPro; IPR011009; Kinase like.

RA Theologis A., Ecker J.R.;
 RN Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
 RA Rudd S., Schoof H., Mayer K.F.X.,
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RP EU Arabidopsis sequencing project;
 RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RL -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC
 DR EMBL; AF361634; AAC32802.1; -;
 DR EMBL; AF592312; CAC42909.1; -;
 DR HSSP; P49137; INXK.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR002048; EF_Hand.
 DR InterPro: IPR011093; EF_Hand_Like.
 DR InterPro: IPR008080; parvalbumin.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR PRINTS; PR01697; PARVALBUMIN.
 DR ProDom; PD000012; EF_Hand; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00054; EFh; 4.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 3.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00109; Serine/threonine-protein kinase; Transferase.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 535 AA; 60309 MW; 56196BB883D79A34 CRC64;
 Query Match 80.4%; Score 1141; DB 2; Length 535;
 Best Local Similarity 79.5%; Pred. No. 4.9e-70;
 Matches 213; Conservative 26; Mismatches 29; Indels 0; Gaps 0;
 QY 7 ISDKYLGRGEGFGITLYCTDRETREALACKSISKRLTAVDVEDVRREVTIMSTL 66
 DB 55 ISLQYDLGRVGRGEGFGITLYCTDRETREALACKSISKRLTAVDVEDVRREVTIMSTL 114
 QY 67 PEHPNVVKLYATYEDNETVHLVMECEGELFGRIVARGHYTERAAATVARTIAEVRMC 126
 DB 115 PKHPNVVSLKSDDEDDAVHIVMECEGELFGRIVARGHYTERAAATVARTIAEVRMC 174
 QY 127 HVGVMHRDLKPENFLFANKKENSALKATDFGLSVLFKGERFETVGSPPYMAPEVLKR 186
 DB 175 HQGVVHRDLKPENFLFANKKETSALKATDFGLSVLFKGERFETVGSPPYMAPEVLKR 234
 QY 187 NYGPEVDVMSAGVILYLLCGVPPFWAETEQQVALAILRGVLDKRDPSQISESAKSLV 246
 DB 235 NYGPEIDVMSAGVILYLLCGVPPFWAETEQQVAQAIIRSDFKRDPPRVSADKDLV 294
 QY 247 KOMLEPDSKYRLTAQOVLDPHPIQNAKK 274
 DB 295 RKMLEPDPKRLTAQVLESHITLNAKK 322
 RESULT 14
 ID Q96294 PRELIMINARY; PRT; 503 AA.
 AC Q96294;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Calcium-dependent protein kinase.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Columbia;
 RA Grellet F., Wu H.-J., Gaubier-Comella P., Berger C., Mares G.,
 RA Delseeny M.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20108326; PubMed=10645728; DOI=10.1023/A:1006395324818;
 RX Comella P., Wu H.-J., Laudie M., Berger C., Cooke R., Delseeny M.,
 RA Grellet F.;
 RT "Fine sequence analysis of 60 kb around the Arabidopsis thaliana AtEm1
 locus on chromosome III.";
 RL Plant Mol. Biol. 41:687-700(1999).
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AF049236; AAC14412.1; -;
 DR EMBL; AF049236; AAC14412.1; -;
 DR PIR; T51156; T51156.
 DR HSSP; P49137; INXK.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR002048; EF_Hand.
 DR InterPro: IPR010983; EF_Hand_Like.
 DR InterPro: IPR011009; Kinase_Like.
 DR InterPro: IPR00719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000012; EF_Hand; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00054; EFh; 3.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00109; Serine/threonine-protein kinase; Transferase.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 503 AA; 56495 MW; 3563C37639B3E916 CRC64;
 Query Match 80.0%; Score 1135; DB 2; Length 503;
 Best Local Similarity 78.0%; Pred. No. 1.2e-69;
 Matches 209; Conservative 31; Mismatches 28; Indels 0; Gaps 0;
 QY 7 ISDKYLGRGEGFGITLYCTDRETREALACKSISKRLTAVDVEDVRREVTIMSTL 66
 DB 50 IEDRYLLDRELGREGFGVLYLCIERSSDDLACKSISKRLTAVDIEDVKEVIMKHL 109
 QY 67 PEHPNVVKLYATYEDNETVHLVMECEGELFGRIVARGHYTERAAATVARTIAEVRMC 126
 DB 110 PKSSIVTLKEACEDDNAVHLMVMECEGELFGRIVARGHYTERAAATVARTIAEVRMC 169
 QY 127 HVGVMHRDLKPENFLFANKKENSALKATDFGLSVLFKGERFETVGSPPYMAPEVLKR 186
 DB 170 HKGVVHRDLKPENFLFANKKENSALKATDFGLSVLFKGERFETVGSPPYMAPEVLKR 229
 QY 187 NYGPEVDVMSAGVILYLLCGVPPFWAETEQQVALAILRGVLDKRDPSQISESAKSLV 246
 DB 230 NYGPEIDVMSAGVILYLLCGVPPFWAETEQQVAQAIIRGVLDKRDPSQISESAKSLV 289
 QY 247 KOMLEPDSKYRLTAQOVLDPHPIQNAKK 274
 DB 290 RKMLEPDPKRLTAQVLESHITLNAKK 317

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OM protein - protein search, using sw model

Run on: October 14, 2005, 10:54:26 ; Search time 166 Seconds
(without alignment)
638.388 Million cell updates/sec

Title: US-08-989-881-2
Perfect score: 1419
Sequence: 1 MANQTQISDKYLGLRELGRG.....TKRLTAQQLVDHPWQNAK 274

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1419	100.0	274	2 AAW49837	Aaw49837 Amino aci
2	1419	100.0	274	4 AAG65757	Aag65757 ATCDPK1a
3	1419	100.0	274	4 AAG65759	Aag65759 ATCDPK1a
4	1318	92.9	274	4 AAG65756	Aag65756 ATCDPK1 k
5	1161	81.8	538	3 AAG43621	Aag43621 Arabidops
6	1161	81.8	538	8 ADN72463	Adn72463 Thale cre
7	1146	80.8	263	7 ABB80250	Abb80250 Fragaria
8	947	66.7	549	5 AAM52842	Aam52842 Physcomit
9	931	65.6	424	3 AAG43622	Aag43622 Arabidops
10	929	65.5	421	3 AAG43623	Aag43623 Arabidops
11	929	65.5	463	3 AAG46565	Aag46565 Arabidops
12	926	65.3	639	5 ABP53637	Abp53637 Maize cal
13	916	64.6	413	4 AAG65755	Aag65755 ATCDPK ki
14	903	63.6	856	3 AAG38599	Aag38599 Arabidops
15	903	63.6	893	3 AAG38598	Aag38598 Arabidops
16	903	63.6	1017	3 AAG38597	Aag38597 Arabidops
17	887.5	62.5	490	8 ADM72386	Adm72386 A. thalia
18	887	62.5	280	4 AAG65758	Aag65758 ATCDPK2 k
19	887	62.5	459	3 AAG29591	Aag29591 Arabidops
20	887	62.5	495	5 AAM48000	Aam48000 Arabidops
21	887	62.5	529	3 AAG29590	Aag29590 Arabidops
22	887	62.5	542	3 AAG29589	Aag29589 Arabidops
23	884	62.3	549	8 ADI45327	Adi45327 Rice isop
24	874	61.6	483	3 AAG31158	Aag31158 Arabidops
25	874	61.6	556	3 AAG31157	Aag31157 Arabidops

26	871	61.4	465	8 ADM72385	Adm72385 Maize CDP
27	865	61.0	501	3 AAG35776	Aag35776 Arabidops
28	865	61.0	501	5 AAM48001	Aam48001 Arabidops
29	861.5	60.7	512	2 AAW93256	Aaw93256 Soybean C
30	819	57.7	569	2 AAR56237	Aar56237 Protein k
31	757	53.3	404	3 AAG46566	Aag46566 Arabidops
32	710	50.0	408	3 AAG31159	Aag31159 Arabidops
33	710	50.0	597	5 AAM52841	Aam52841 Physcomit
34	706	49.8	425	3 AAG35777	Aag35777 Arabidops
35	706	49.8	523	8 ADN73153	Adn73153 Thale cre
36	699	49.3	523	3 AAG10101	Aag10101 Arabidops
37	697	49.1	623	4 AAB85583	Aab85583 Rice CDPK
38	697	49.1	623	5 ABP53630	Abp53630 Maize cal
39	690	48.6	625	5 ABP53638	Abp53638 Maize cal
40	689	48.6	483	7 ADC07764	Adc07764 Rice prot
41	688	48.5	599	7 ADL06615	Adl06615 Tobaccoc
42	685	48.3	378	3 AAG46567	Aag46567 Arabidops
43	682	48.1	386	8 ADM72366	Adm72366 Soybean C
44	676	47.6	576	5 ABP53639	Abp53639 A. thalia
45	648.5	45.7	416	8 ADM72364	Adm72364 Soybean C

ALIGNMENTS

RESULT 1
AAW49837
ID AAW49837 standard; protein; 274 AA.
XX
AC AAW49837;
XX
XX
DT 27-AUG-2003 (revised)
DT 12-OCT-1998 (first entry)
XX
XX

DE Amino acid sequence of ATCDPK1a PK domain.
XX
ATCDPK1a; protein kinase; PK; tolerance; drought; salinity; cold; heat;
KW fruit; ornamental; vegetable; cereal; field crops.
XX

OS Arabidopsis sp.

XX WO9826045-A1.

XX 18-JUN-1998.

PF 12-DEC-1997; 97WO-US023019.

PR 13-DEC-1996; 96US-0032966P.

XX (GEHO) GEN HOSPITAL CORP.

XX Sheen J;

DR WPI; 1998-348509/30.

XX N-PSDB; AAV36878.

PT Protecting plants against environmental stress - by introducing protein kinase domain-containing gene, calcium dependent protein kinase gene or calcium/calmodulin-dependent gene.

Claim 22; Fig 5; 62pp; English.

This is the amino acid sequence of the ATCDPK1a protein kinase (PK) domain isolated from the Arabidopsis cDNA library, and used in the method of the invention to protect plants against environmental stress. The methods can be used for improving the tolerance of plants to environmental stresses such as drought, salinity, cold and heat. They provide for increased production efficiency, as well as for improvements in quality and the yield of crop plants and ornamentals. The methods contribute to the production of high quality and high yield agricultural products, e.g. fruits, ornamentals, vegetables, cereals, and field crops. (Updated on 27-AUG-2003 to correct OS field.)

XX

CC library member is expressed in the plant protoplasts; and (2) screening
 CC the protoplasts to determine whether the amount of gene expression of the
 CC reporter gene construct changes in response to the expression of the
 CC library members, a change in gene expression of the reporter gene
 CC construct identifying the gene product expressed by the library member as
 CC 1 that modulates expression of the gene of interest. The present sequence
 CC represents the amino acid sequence of Arabidopsis calcium dependant
 CC protein kinase (CDPK) ATCDPK1a PK domain
 XX Sequence 274 AA;

Query Match 100.0%; Score 1419; DB 4; Length 274;
 Best Local Similarity 100.0%; Pred. No. 5.4e-146;
 Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANOTQISDKYILGRELGRGFGITVCTDRETRALACKSISKRLRTAVDVEDVRREV 60
 DB 1 MANOTQISDKYILGRELGRGFGITVCTDRETRALACKSISKRLRTAVDVEDVRREV 60
 QY 61 TIMSTLPEHPNVVVKLKYEDNETVHLMELCEGELFGRIIVARGHYTERAAATVARTIA 120
 DB 61 TIMSTLPEHPNVVVKLKYEDNETVHLMELCEGELFGRIIVARGHYTERAAATVARTIA 120
 QY 121 EYVRMCHVNGVMHRDLKPENFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYNA 180
 DB 121 EYVRMCHVNGVMHRDLKPENFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYNA 180
 QY 181 PEVLKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPWSQISE 240
 DB 181 PEVLKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPWSQISE 240
 QY 241 SAKSLVKOMLEPDPSTKRLTAQQVLDHPWIONAKK 274
 DB 241 SAKSLVKOMLEPDPSTKRLTAQQVLDHPWIONAKK 274

RESULT 4
 AAG65756
 ID AAG65756 standard; protein; 274 AA.

XX AC AAG65756;
 XX DT 07-JAN-2002 (first entry)
 XX DE ATCDPK1 kinase domain sequence.
 XX KW Plant protoplast; gene expression; Arabidopsis; PK; CDPK; ATCDPK1;
 XX OS calcium activated protein kinase; calcium dependant protein kinase.
 XX PN Arabidopsis thaliana.

XX WO200168920-A1.

XX PD 20-SEP-2001.

XX PF 13-MAR-2001; 2001WO-US007999.

XX PR 13-MAR-2000; 2000US-0189074P.

XX PA (GENO) GEN HOSPITAL CORP.

XX PI Sheen J;

XX DR WPI; 2001-611395/70.

XX PT Using plant protoplast expression systems for rapidly screening libraries
 XX of nucleic acids to identify gene that modulate expression of target
 XX genes.

XX PS Example; Fig 3B; 95pp; English.

XX CC The invention provides a high through-put assay for rapidly screening a
 CC library of nucleic acid molecules to identify a gene product that

CC modulates expression of a gene of interest in plant protoplasts. The
 CC method comprises: (1) introducing into 1 or more plant protoplasts: (a) a
 CC reporter gene construct operably linked to a promoter of a gene of
 CC interest; and (b) a member of a library of nucleic acid molecules (the
 CC library member) is expressed in the plant protoplasts; and (2) screening
 CC the protoplasts to determine whether the amount of gene expression of the
 CC reporter gene construct changes in response to the expression of the
 CC library members, a change in gene expression of the reporter gene
 CC construct identifying the gene product expressed by the library member as
 CC 1 that modulates expression of the gene of interest. The present sequence
 CC represents the amino acid sequence of Arabidopsis calcium dependant
 XX protein kinase (CDPK) ATCDPK1 kinase domain
 XX Sequence 274 AA;

Query Match 92.9%; Score 1318; DB 4; Length 274;
 Best Local Similarity 92.0%; Pred. No. 5.8e-135;
 Matches 252; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 MANOTQISDKYILGRELGRGFGITVCTDRETRALACKSISKRLRTAVDVEDVRREV 60
 DB 1 MSNQTQISDKYILGRELGRGFGITVCTDRETRALACKSISKRLRTAVDVEDVRREV 60
 QY 61 TIMSTLPEHPNVVVKLKYEDNETVHLMELCEGELFGRIIVARGHYTERAAATVARTIA 120
 DB 61 AIMSTLPEHPNVVVKLKYEDNETVHLMELCEGELFGRIIVARGHYTERAAATVARTIA 120
 QY 121 EYVRMCHVNGVMHRDLKPENFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYNA 180
 DB 121 EYVRMCHVNGVMHRDLKPENFLFANKKENSALKKIDFGLSVLPKGERFTEIVGSPYYNA 180
 QY 181 PEVLKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPWSQISE 240
 DB 181 PEVLKRNYPGVVDVMSAGVILYLLCGVPPFWAETEQGVVALAILRGVLDPKRDPWSQISE 240
 QY 241 SAKSLVKOMLEPDPSTKRLTAQQVLDHPWIONAKK 274
 DB 241 SAKSLVKOMLEPDPSTKRLTAQQVLDHPWIONAKK 274

RESULT 5
 AAG43621

ID AAG43621 standard; protein; 538 AA.

XX AC AAG43621;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 54544.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
 XX hybridisation assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 23-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 29-MAR-1999; 99US-0126264P.

XX PR 01-APR-1999; 99US-0126785P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130443P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131144P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
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PR 14-MAY-1999; 99US-0134370P.
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PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
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PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140961P.
PR 30-JUN-1999; 99US-0141287P.
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PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
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PR 15-JUL-1999; 99US-0144005P.
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PR 19-JUL-1999; 99US-0144325P.
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PR 20-JUL-1999; 99US-0144352P.
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PR 21-JUL-1999; 99US-0144814P.
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PR 23-JUL-1999; 99US-0145145P.
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PR 23-JUL-1999; 99US-0145224P.
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PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 06-AUG-1999; 99US-0147303P.
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PR 18-AUG-1999; 99US-0149426P.
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PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
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PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-01511080P.
PR 31-AUG-1999; 99US-01511303P.
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PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
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PR 28-SEP-1999; 99US-0156458P.
PR 28-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
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PR 08-OCT-1999; 99US-0158232P.
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PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.

fungal growth; development; inhibition.

Fragaria x ananassa.

WO2003076582-A2.

18-SEP-2003.

06-MAR-2003; 2003WO-US006935.

06-MAR-2002; 2002US-0362008P.

21-MAR-2002; 2002US-0366504P.

(SYGN) SYNGENTA PARTICIPATIONS AG.

(REGC) UNIV CALIFORNIA.

(JUDE/) JUDELSON H S.

Judelson HS;

WPI; 2003-731821/69.

Identifying a fungicidal compound comprises combining a polypeptide with the compound to be tested with the ability to bind, or to inhibit the activity of the polypeptide under conditions conducive to binding or inhibition.

Disclosure; Fig 3c; 105pp; English.

The sequences given in ABB80245-52 shows calcium/calmodulin-dependant protein kinases (CaMK) from various animals which are included for comparison with the P. infestans CaMK of the invention. The CaMK gene is expressed as an intron-lacking transcript bearing 5' and 3' untranslated regions of 50 and 45 nt, respectively. CaMK plays a role in fungal growth and development. The CaMK protein may be used in the method of the invention for identifying a fungicidal compound. The method comprises combining the CaMK polypeptide with the compound to be tested with the ability to bind or to inhibit the activity of the polypeptide under conditions conducive to binding or inhibition. The method is useful for identifying compounds that interact with or inhibit the proteins essential for fungal growth, which are thus useful as fungicides. The proteins are useful for in vitro assays for screening fungicidal chemicals whose targets has not been identified to determine if they inhibit protein activity, and for elucidating the complex structures of these molecule and to further characterize their association with known inhibitors in order to rationally design new inhibitory herbicides

Sequence 263 AA;

Query Match 80.8%; Score 1146; DB 7; Length 263;
Best Local Similarity 81.0%; Pred. No. 3.4e-116; Mismatches 27; Indels 0; Gaps 0;
Matches 213; Conservative 23;

Qy 11 YILGRELGRGFGITYLCTDRETRALACKSISKRKLRTAVDVEDVREVTINSTLPEHP 70
Db 1 YELGRELGRGFGITYLCTDRTATNENYACKSISKQKLTAVDIEDVREVEIMKHLPGHP 60
Qy 71 NVVKLKATYENETVHLVWMLCEGELPGRIVARGHYTERAAATVARTIARVVRMCHVNG 130
Db 61 NIVSLKDTYEDDNVHLVWMLCEGELPDRIVSRGHYTERAAATVARTIARVVRMCHVNG 120
Qy 131 VMHRLDKPENFLFANKENSALKAKIDFGLSVLFKPGERTFIVGSPYMAPEVLKRYNGP 190
Db 121 VMHRLDKPENFLFANKKETAPLKADPGLSVVFFKPGERTFIVGSPYMAPEVLKRYNGP 180
Qy 191 EVDVMSAGVILYILLCGVPPFWAETEQQVALAILRGVLDKRDQWQSQISAKSLVKQML 250
Db 181 EVDVMSAGVILYILLCGVPPFWAETEQQVAQAIIRSVVDFKRDQWPKVSDNAKDLVKQML 240
Qy 251 EPDSTKRLTAQOVLDPHPIQNAK 273
Db 241 DDPKRLTAQOVLDPHTWLQNAK 263

RESULT 8

AAM52842

ID AAM52842 standard; protein; 549 AA.

XX AC AAM52842;

XX DT 22-FEB-2002 (first entry)

XX DE Physcomitrella patens CPK-2 protein, SEQ ID NO:39.

XX KW Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;
KW PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;
KW PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;
KW casein kinase homologue-3; CK-3; mitogen-activated protein kinase;
KW MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;
KW MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;
KW calcium-dependent protein kinase-2; CPK-2; overexpression;
KW environmental stress; salinity; drought; temperature; tolerance;
KW transgenic plant; EST; expressed sequence tag.

XX OS Physcomitrella patens.

XX PN WO200177356-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-US011435.

XX PR 07-APR-2000; 2000US-0196001P.

XX PA (BADI) BASF PLANT SCI GMBH.

XX PI Da Costa E SilvaO, Bohnert HJ, Van Thiel N, Chen R;

XX PT Sarria-Millan R;

XX DR WPI; 2002-049153/06.

XX DR N-PSDB; ABA91081.

XX FT New protein, useful for increasing tolerance to environmental stress,
PT comprises a Protein Kinase Stress-Related Protein selected from Protein
PT Kinases, Casein kinase homologs, MAP kinases or Calcium dependent protein
PT kinases.

XX PS Claim 13; Fig 3M; 154pp; English.

XX CC Sequences AAM52830-AAM52842 represent novel protein kinase stress-related
CC proteins (PKSRPs) from the moss Physcomitrella patens, and sequences
CC ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA
CC sequences were obtained from expressed sequence tags (ESTs; ABA91056-
CC ABA91068) derived from Physcomitrella patens cDNA libraries. The PKSRPs
CC of the invention comprise protein kinase-6 (PK-6), protein kinase-7 (PK-
CC 7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase
CC homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase
CC homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2), MAP
CC kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5), calcium-
CC dependent protein kinase-1 (CPK-1) and calcium-dependent protein kinase-
CC 2 (CPK-2). When overexpressed, the PKSRPs are able to confer tolerance to
CC environmental stresses such as salinity, drought, temperature, metal,
CC chemical, pathogenic and oxidative stress. Physcomitrella patens PKSRP
CC nucleic acids may be used to generate transgenic plants and seeds with
CC increased tolerance to salinity, drought and temperature. The transgenic
CC plants generated can be monocots or dicots and are especially maize,
CC wheat, rye, oat, triticale, rice, barley, cotton, rapeseed, cassava,
CC sunflower, tagetes, leguminous plants (e.g., soybean, peanut, vicia,
CC species, alfalfa), solanaceous plants (e.g., potato, tobacco, aubergine,
CC pepper, tomato), coffee, cacao, tea, Salix species, oil palm, coconut,
CC perennial grasses and forage crops. The PKSRP nucleotide and proteins may
CC also be used in evolutionary and protein structural studies and as
CC markers for specific regions of the genome

XX SQ Sequence 549 AA;

Query Match 66.7%; Score 947; DB 5; Length 549;

Best Local Similarity 66.2%; Pred. No. 5.7e-94;		Matches 176; Conservative 35; Mismatches 55; Indels 0; Gaps 0;	
Qy	5	TSQSDKYLGRGREGFGITYLCTDRETRREALACKSISKRKLTAVDVEDVREVTIMS 64	
Db	87	SDIQSYILGRELGRGQFGVYTLCTDKMTNEAYACKSLKSKEDIEDVKREYQIMH 146	
Qy	65	TLPEHPNVKLTATYEDNETVHLVMBELCEGGLFGRIVARGHYTERAAATVARTIAEVVR 124	
Db	147	HLSGTNIIVLVKDVFDKSHVHLVMBELCAGGELFDRIIAKGYHSERAAADMCRVINVVH 206	
Qy	125	MCHVNGMHRDLKPENFLFANKKENSALKKAIDFGLSVLPKPGERFTEIVGSPYYMAPEVL 194	
Db	207	RCHSLGVFHRDLKPENFLKASKAEDAPLKATDFGLSTFFPKPGDVFDIVGSAYVVAPEVL 266	
Qy	185	KRNYGPEVDVWSAGVILYLLCGVPPFWAETEGQVALAILRGVLDPKRDPWSOISSAKS 244	
Db	267	KRSYGPEADVWSAGVIVYLLCGVPPFWAETEGQIFDAVLKGHIDFENDFPKPKISNGAKD 326	
Qy	245	LVKOMLEPDSTKRLTAQOVLDPHPIQ 270	
Db	327	LVRKMLNPVKRLTAQOVLNHPWMK 352	
RESULT 9			
AAG43622			
ID	AAG43622 standard; protein; 424 AA.		
AC	AAG43622;		
XX			
DT	18-OCT-2000 (first entry)		
XX			
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 54545.		
KW	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-00301439.		
XX			
PR	25-FEB-1999;	99US-0121825P.	99US-0134768P.
PR	05-MAR-1999;	99US-0123180P.	99US-0134941P.
PR	09-MAR-1999;	99US-0123548P.	99US-0135124P.
PR	23-MAR-1999;	99US-0125788P.	99US-0135353P.
PR	25-MAR-1999;	99US-0126264P.	99US-0135629P.
PR	29-MAR-1999;	99US-0126785P.	99US-0136021P.
PR	01-APR-1999;	99US-0127462P.	99US-0136392P.
PR	06-APR-1999;	99US-0128234P.	99US-0136782P.
PR	08-APR-1999;	99US-0128714P.	99US-0137222P.
PR	16-APR-1999;	99US-0129845P.	99US-0137528P.
PR	19-APR-1999;	99US-0130077P.	99US-0137502P.
PR	21-APR-1999;	99US-0130449P.	99US-0137724P.
PR	23-APR-1999;	99US-0130510P.	99US-0138094P.
PR	28-APR-1999;	99US-0130891P.	99US-0138540P.
PR	30-APR-1999;	99US-0131449P.	99US-0138847P.
PR	04-MAY-1999;	99US-0132407P.	99US-0139119P.
PR	05-MAY-1999;	99US-0132484P.	99US-0139452P.
PR	06-MAY-1999;	99US-0132485P.	99US-0139453P.
PR	06-MAY-1999;	99US-0132486P.	99US-0139492P.
PR	07-MAY-1999;	99US-0132487P.	99US-0139454P.
PR	11-MAY-1999;	99US-0132863P.	99US-0139455P.
PR	14-MAY-1999;	99US-0134256P.	99US-0139456P.
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PR	14-MAY-1999;	99US-0134219P.	99US-0139458P.
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PR	14-MAY-1999;	99US-0134370P.	99US-0139460P.

PR	18-MAY-1999;	99US-0134768P.
PR	19-MAY-1999;	99US-0134941P.
PR	20-MAY-1999;	99US-0135124P.
PR	21-MAY-1999;	99US-0135353P.
PR	24-MAY-1999;	99US-0135629P.
PR	25-MAY-1999;	99US-0136021P.
PR	27-MAY-1999;	99US-0136392P.
PR	01-JUN-1999;	99US-0136782P.
PR	03-JUN-1999;	99US-0137222P.
PR	04-JUN-1999;	99US-0137528P.
PR	07-JUN-1999;	99US-0137502P.
PR	08-JUN-1999;	99US-0137724P.
PR	10-JUN-1999;	99US-0138094P.
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PR	21-JUL-1999;	99US-0144814P.
PR	21-JUL-1999;	99US-0145086P.
PR	21-JUL-1999;	99US-0145088P.
PR	22-JUL-1999;	99US-0145085P.
PR	22-JUL-1999;	99US-0145087P.
PR	22-JUL-1999;	99US-0145089P.
PR	22-JUL-1999;	99US-0145192P.
PR	23-JUL-1999;	99US-0145145P.
PR	23-JUL-1999;	99US-0145218P.
PR	23-JUL-1999;	99US-0145224P.
PR	26-JUL-1999;	99US-0145276P.
PR	27-JUL-1999;	99US-0145913P.
PR	27-JUL-1999;	99US-0145918P.

PR 27-JUL-1999;	99US-0145919P.
PR 28-JUL-1999;	99US-0145951P.
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PR 04-AUG-1999;	99US-0147204P.
PR 04-AUG-1999;	99US-0147302P.
PR 05-AUG-1999;	99US-0147192P.
PR 05-AUG-1999;	99US-0147260P.
PR 06-AUG-1999;	99US-0147303P.
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Db 61	VQVCHKGVMHRDLKPFNFIFGNKKETAPLKAIDFGLSVFVKPGERTFTEIVGSPYYMAPE 120
Qy 183	VLKRNYPGVDSAGVILYLLCGVPPFWAETEQGVALLRGLDFKRDPMQISESA 242
Db 121	VLKRNYPGVDIWSAGVILYLLCGVPPFWAETEQGVAQAIIRSVLDFRRDPWPKVSENA 180
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KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
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PN	06-SEP-2000.
PD	25-FEB-2000; 2000EP-00301439.
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AC AAG46565;
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX
XX 06-SEP-2000.
XX
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
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XX 23-MAR-1999; 99US-0125788P.
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Best Local Similarity 63.6%; Score 903; DB 3; Length 856;

Best Local Similarity 63.6%; Pred. No. 7.2e-89;

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DT	18-OCT-2000 (first entry)

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KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
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Query Match 63.6%; Score 903; DB 3; Length 893;

Best Local Similarity 63.6%; Pred. No. 7.6e-89;
Matches 173; Conservative 29; Mismatches 58; Indels 12; Gaps 1;

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Search completed: October 14, 2005, 11:05:41
Job time : 170 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 10:40:31 ; Search time 21 Seconds
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973.993 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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5	871	61.4	464	3	US-08-459-595A-22
6	871	61.4	464	3	US-08-459-504B-22
7	871	61.4	464	3	US-08-459-444-22
8	871	61.4	464	3	US-09-547-422-22
9	871	61.4	464	4	US-09-988-462-22
10	861.5	60.7	463	1	US-07-951-715A-25
11	861.5	60.7	463	2	US-08-459-448A-25
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ALIGNMENTS

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; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
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; TYPE: PRT
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Db	149	LKDKYSLGRRLCQQQFGTTHLCVERATGKELACKSLKRLGSDDDVEDVREIOMHL	208				
Qy	67	PEHPNVKLKATYEDNETVHLMELCGGELFGFRIVARGHYTERAAATVARTIAEVVRC	126				
Db	209	AGHPSVVGIRGAYEDAVAVHLMELCGGELFDRIVRRGHYTERKAEALRVIVGVWEC	268				
Qy	127	HVNGVHRDLKPEFLFANKKENSALKADGLSLFKPGRFTEIVGSPYMAPEVLKR	186				
Db	269	HSMGVHRDLKPEFLFADHSEEAALKTIDFGLSIFRPGQIFIDVVGSPYMAPEVLKR	328				
Qy	187	NYGPEVDVWSAGVLYILLCGVPPFWAETEGVALAILRGVLDKFRDPWSQISESAKGLV	246				
Db	329	RYGPEADVWSAGVLYILLCGVPPFWAETEGVALAILRGVLDKFRDPWSQISESAKGLV	388				
Qy	247	KQMLEPSTKRLTAQOVLDPHWIQ	270				
Db	389	RRMLVDRPKRLTAHEVLRHPWQ	412				
RESULT 2							
US-09-854-731-17							
; Sequence 17, Application US/09854731							
; Patent No. 6794561							

GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/092,438
PRIOR FILING DATE: July 10, 1998
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 639
TYPE: PRT
ORGANISM: Zea mays
US-09-854-731-17

Query Match 65.3%; Score 926; DB 4; Length 639;
Best Local Similarity 65.5%; Pred. No. 1.6e-86;
Matches 173; Conservative 31; Mismatches 60; Indels 0; Gaps 0;

Qy 7 ISDKYILGRLGEGFITYLCTDRETRALACKSISKRKLRTAVDVEDVRREVTIMSTL 66
Db 149 LKDYSLGRLGQGFQTHLCVERATGKELACKSILKRLGSDDDVEDVREIQIMHLL 208

Qy 67 PEHNVVVKLKYEDNETVHLMELCGGELFGRIVARHYTERAAATVARTIAEVVVMC 126
Db 209 AGHPSVVGIRGAYEDAVAVHLMELCGGELFGRIVARHYTERKAAELARVIVGVVEAC 268

Qy 127 HVNGVMHRLDKPENFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYMAPEVLKR 186
Db 269 HSMGVHRLDKPENFLFADHSEEAALKTIDFGLSIFRPGQIFDVGSPYVAPEVLKK 328

Qy 187 NYGPEVDWSAGVILYLLCGVPPFAETEGQVALAILRGVLDPKRDPWQISSEAKSLV 246
Db 329 RYGPEDWWSAGVILYLLCGVPPFAEENEGQIFEEVILHRLDSESPWPSISDGAKDLV 388

Qy 247 KMLEPDSKRLTAQOVLDPHIQ 270
Db 389 RMLVDRPKRLTAHEVLRHPWQ 412

RESULT 3
US-07-951-715A-22
Sequence 22, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note= "derived protein sequence of
OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-07-951-715A-22

Query Match 61.4%; Score 871; DB 1; Length 464;
Best Local Similarity 63.1%; Pred. No. 4.8e-81;
Matches 164; Conservative 31; Mismatches 65; Indels 0; Gaps 0;

Qy 11 YILGRLGEGFITYLCTDRETRALACKSISKRKLRTAVDVEDVRREVTIMSTLPEHP 70
Db 13 YSMGKELGRGQFGVTHLCTHRTSGELACKTIARKLAAREDVDDVRREVOIMHLLSGOP 72

Qy 71 NVVKLKATYEDNETVHLMELCGGELFGRIVARHYTERAAATVARTIAEVVVMCHVNG 130
Db 73 NVVGLRGAYEDKQSVHLMELCAGGELFDRILARGQYTERGAELRLAIQIVHTCHSMG 132

Qy 131 VMHRLDKPENFLFANKKENSALKAIIDFGLSVLPKPGERFTEIVGSPYMAPEVLKRYGP 190
Db 133 VMHRLDKPENFLFLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYYIAPEVLKRYGP 192

Qy 191 EVDVWSAGVILYLLCGVPPFAETEGQVALAILRGVLDPKRDPWQISSEAKSLVKQML 250
Db 193 EADIVSVGVNLYIFLAGVPPFAENENGIFTAILRGOLDLSSEPPWPHISPGAKDLVKQML 252

Qy 251 EPDSTKRLTAQOVLDPHIQ 270
Db 253 NINPKRLTAQOVLDPHIQ 272

RESULT 4
US-08-459-448A-22
Sequence 22, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.

APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note= "derived protein sequence of
pollen specific CDPK as disclosed in Figure 34."
US-08-459-448A-22

Query Match 61.4%; Score 871; DB 2; Length 464;
Best Local Similarity 63.1%; Pred. No. 4.8e-81;
Matches 164; Conservative 31; Mismatches 65; Indels 0; Gaps 0;
Qy 11 YILGRLGRGFGTYLCTDRETRALACKSISKRLTAVDVEDVRREVTIMSLPDPHP 70
Db 13 YSMGKELRGQFVTHLCTHRTSGEKLAKTIAKLAAREDDVDREVQIMHLSGP 72
Qy 71 NVVKLKATYEDNEVHLVWELCEGELFGRIVARHYTERAAATVARTIAEVRMCHVNG 130
Db 73 NVVGLRGAYEDKQSVHLVWELCAGGELFDRIIARGQYTERGAALLRAIVQIVTCHSMG 132
Qy 131 VVHRLDKPENLFANKKENSALKATDFGLSVLFKPGFRFTVGVSPYYMAPEVLKRYNGP 190
Db 133 VVHRLDKPENLLSKSDAPLKAATDFGLSVFFKEGELLRLDIVGSAYTIAEVLKRYGP 192
Qy 191 EVDVMSAGVILYLLCGVPPFPAETEOGVVALAILRGVLDKRDPPWSQISESAKSLVKOML 250

Db 193 EADIWSVGVMLYIFLAGVPPFPAENENGIFTAILRGQLDLSESPHISPGAKOLVKOML 252
Qy 251 EPDSTKELTAQOVLDPHIQ 270
Db 253 NINPKERLTAFQVLNHPWIK 272
RESULT 5
US-08-459-595A-22
; Sequence 22, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
FORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note= "derived protein sequence of
OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
-459-504B-22
ry Match 61.4%; Score 871; DB 3; Length 464;

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11 YILGRLGRGBGIIYVLCTDRTREALACKSISKRLRTAVDVEDVRRVETIMSTLPEHP 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
13 YSMKGLRGQGFVTHLCTHRTSGEKLACKTKAKRLAAREDDVDRREVQIMHHLGGOP 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
71 NVVKKATYEDNETVHLMVCEGGEGLFGRIVARGHYTERAAATVARTTAAEVRVMCHVNG 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
73 NVVGLRGATYEDKQSVHLMVCEGGEGLFDRITARGOYTERGAELLRAIVQVHTCHSMG 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
131 VMHRDLKPENFUIPANKKENSALKATDFGLSVLUFKPGERFETIVGSGYMAPEVLKKNYGP 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
133 VMHRDIKPENFLLSKDEAPLAKATDFGLSVFKEGELLRDIVGSAIYTAPEVLKRYKGP 192
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
191 EVDVWSAGVILYILLCGVPPFWAETEOGVALAILRGVDFKRDPMPOISSESAKSLVKQML 250
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
193 EADINSVGMVLIYFLAGVPPFWAENENGIFTAILRGQLDLSSEPWFHISPGAKDLVKKML 252
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 EPDSTKRLTAQQVLDHPWIO 270
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
253 NINPKERLTAQVNLHPWIK 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

T 7
-459-444-22
Sequence 0, Application US/08459444A
ent No. 6121014
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauris, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 6121014artis Agribusiness Biotechnology Research,
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC

COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-459-444-22

Query Match 61.4%; Score 871; DB 3; Length 464;
Best Local Similarity 63.1%; Pred. No. 4.8e-81;
Matches 164; Conservative 31; Mismatches 65; Indels 0; Gaps 0;
Qy 11 YILGRLGRGEGITVLTCTDRETRALACKSISKRLTAVDVEDVRREVTIMSTLPEHP 70
Db 13 YSMGKELGRGQGVTHLCTHRTSGEKLACKTIARKLAAAREDDVDVREVOIMHLSGQP 72
Qy 71 NVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIAEVRMCHVNG 130
Db 73 NVVGLRGAYEDKQSVHLMELCAGGELFDRIIARGQYTERGAELLRAIVQIVHTCHSMG 132
Qy 131 VMHRDLKPNFLFANKKENSALKAIIDFGLSVLFKPGERFTEIVGSPYMAPEVLKRNYP 190
Db 133 VMHRDIKPNFLLSKDEADAPLKATDFGLSVFFKEGELLRDIVGSAYYIAEVLKRYGP 192
Qy 191 EVDVWSAGVILYLLCGVPPFWAETEOGVVALILRGVLDKRDPSQISESAKSLVKOML 250
Db 193 EADIWSGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPPWPHISPGAKDLVKKML 252
Qy 251 EPDSTKRLTAQQLDHPWIQ 270
Db 253 NINPKERLTAQVLNHPWIK 272

RESULT 8
US-09-547-422-22
Sequence 0, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.

Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauais, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-547-422-22
Query Match 61.4%; Score 871; DB 3; Length 464;
Best Local Similarity 63.1%; Pred. No. 4.8e-81;
Matches 164; Conservative 31; Mismatches 65; Indels 0; Gaps 0;
Qy 11 YILGRLGRGEGITVLTCTDRETRALACKSISKRLTAVDVEDVRREVTIMSTLPEHP 70
Db 13 YSMGKELGRGQGVTHLCTHRTSGEKLACKTIARKLAAAREDDVDVREVOIMHLSGQP 72
Qy 71 NVVKLKATYEDNETVHLMELCEGELFGRIVARGHYTERAAATVARTIAEVRMCHVNG 130
Db 73 NVVGLRGAYEDKQSVHLMELCAGGELFDRIIARGQYTERGAELLRAIVQIVHTCHSMG 132
Qy 131 VMHRDLKPNFLFANKKENSALKAIIDFGLSVLFKPGERFTEIVGSPYMAPEVLKRNYP 190
Db 133 VMHRDIKPNFLLSKDEADAPLKATDFGLSVFFKEGELLRDIVGSAYYIAEVLKRYGP 192
Qy 191 EVDVWSAGVILYLLCGVPPFWAETEOGVVALILRGVLDKRDPSQISESAKSLVKOML 250
Db 193 EADIWSGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPPWPHISPGAKDLVKKML 252

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
US-07-951-715A-25

Query Match 60.7%; Score 861.5; DB 1; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

QY 1 MANQTQ-ISKYILGRELGRGEGITVLTCTDRETRALACKSISKRLKRTAVDVEDVRE 59
DB 2 LPQRTQNIREVYEVGRKLGQGGQFTTCTRRASGGKFAKSIIPKRLCKEDYEDVWRE 61
QY 60 VTINSTLPEHPNVVVKLKYATYEDNETVHLVWELCEGGEFGGRIVARGHYTERAAATVARTI 119
DB 62 IQIMHHLSEHANVVRIGTYEDSTAVHLVWELCEGGEFGFDRIVQKGYHSEQAARLIKTI 121
QY 120 AEVVRMCHVNGVWHRDLKPNFLPANKKENSALKAIIDFGLSVLPKPGSRFTIIVGSPYYM 179
DB 122 VEVVEACHSLGVMHRDLKPNFLDIDEDAKLKATDFGLSVFYKPGSFCDVVGSPYYV 181
QY 180 APEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETOGVALAILRGVLDKFRDPWSQIS 239
DB 182 APEVLKRLYGPESDVWSAGVILYILLSGVPPFWAESPFGIPQIILLGLKLDHFSEWPSIS 241
QY 240 ESAKSLVKQMLEPDSKRLTAQOVLDPHWI 269
DB 242 DSAKDLIRKMLDQNPKRLTAHEVLRHPWI 271

RESULT 11

US-08-459-448A-25
; Sequence 25, Application US/08459448A
; Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.

APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF INVENTION: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5859336artis Corporation

STREET: Patent & Trademark Dept., 520 White Plains

STREET: Rd., POB 2005

CITY: Tarrytown

STATE: New York

COUNTRY: USA

ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459.448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951.715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772.027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
US-08-459-448A-25

Query Match 60.7%; Score 861.5; DB 2; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

QY 1 MANQTQ-ISKYILGRELGRGEGITVLTCTDRETRALACKSISKRLKRTAVDVEDVRE 59
DB 2 LPQRTQNIREVYEVGRKLGQGGQFTTCTRRASGGKFAKSIIPKRLCKEDYEDVWRE 61
QY 60 VTINSTLPEHPNVVVKLKYATYEDNETVHLVWELCEGGEFGGRIVARGHYTERAAATVARTI 119
DB 62 IQIMHHLSEHANVVRIGTYEDSTAVHLVWELCEGGEFGFDRIVQKGYHSEQAARLIKTI 121
QY 120 AEVVRMCHVNGVWHRDLKPNFLPANKKENSALKAIIDFGLSVLPKPGSRFTIIVGSPYYM 179
DB 122 VEVVEACHSLGVMHRDLKPNFLDIDEDAKLKATDFGLSVFYKPGSFCDVVGSPYYV 181
QY 180 APEVLKRNYPGEVDVWSAGVILYILLCGVPPFWAETOGVALAILRGVLDKFRDPWSQIS 239
DB 182 APEVLKRLYGPESDVWSAGVILYILLSGVPPFWAESPFGIPQIILLGLKLDHFSEWPSIS 241
QY 240 ESAKSLVKQMLEPDSKRLTAQOVLDPHWI 269
DB 242 DSAKDLIRKMLDQNPKRLTAHEVLRHPWI 271

RESULT 12

US-08-459-595A-25
; Sequence 25, Application US/08459595A
; Patent No. 6018104

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-08-459-595A-25

Query Match 60.7%; Score 861.5; DB 3; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

Qy 1 MANQTO-ISKYILGRSLGEGFITYLCTDRETRALACKSISKRLRTAVDVEDVRE 59
Db 2 LPQRTQNIREVYEGVKLGQGFQFTTECTRRASGGKFPKRLCKEYEDVRE 61
Qy 60 VTMTSLPEHPNVKLTATVEDNETHVLMELCEGGLFGRIVARGHYTERAAATVARTI 119
Db 62 IQIMHLSHANVVRIGSTVEDSTAVHLMELCEGGLFDRIVQKHYSERQARLKI 121
Qy 120 AEVVRMCHVNGVHMRDLKPNFLPANKKENSALKAFDGLSVLPKQERTTEIVGSPY 179
Db 122 VEVVEACHSLGVHMRDLKPNFLPDTTIDEAKLKATDFGLSVFYKPGESFCDVVGSPY 181

Qy 180 APEVLKRNYPGVDSAGVILYLLCGVPPFWAETEGVALAILRGVLDKRDPMHQSIS 239
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Qy 240 ESAKSLVKOMLEPDSKRLTAQOVLDPHMI 269
Db 242 DSAKDLIRKMLDONPKTRLTAHEVLRHPMI 271
RESULT 13
US-08-459-504B-25
Sequence 25, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:

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; NAME/KEY: Protein
; LOCATION: 1..463
; OTHER INFORMATION: /note= "protein sequence for
; OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-08-459-504B-25

Query Match 60.7%; Score 861.5; DB 3; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

Qy 1 MANQTO-ISKYILGRELGRGEGITYLCTDRETREALACKSISKRLRTAVDVEDVRE 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 LPORTQNIREVYEVGRKLGQGFQGTTFCTRRASGKGFACKSIKPKLLCKEDYEDVRE 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 60 VTINSTLPEHNPVVKLKYATYEDNETVHLVLMELCEGGEFGRIIVARGHYTERAAATVARTI 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 IQIMHHLSEHANVVRIEGTSTDAVHLVLMELCEGGEFGRIIVOKGHYSERQAARLTKTI 121
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Qy 120 AEVVRMCHVNGVHRDLKPNFLFANKKENSALKKAIDFGLSVLPKPGERFTEIVGSPYYM 179
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Qy 180 APEVLKRNYPEDVMSAGVILYLLCGVPPFWAETEOGVVALAILRGVLDPKRDPWQSIS 239
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Db 182 APEVLKRLYGPESDVMSAGVILYLLSGVPPFWAESPFGIFRQILLGKLDHSPWPSPIS 241
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RESULT 14
US-08-459-444-25
; Sequence 0, Application US/08459444
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
```

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; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "protein sequence for
; soybean CDPK as shown in Figure 34."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-459-444-25

Query Match 60.7%; Score 861.5; DB 3; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

Qy 1 MANQTO-ISKYILGRELGRGEGITYLCTDRETREALACKSISKRLRTAVDVEDVRE 59
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Db 2 LPORTQNIREVYEVGRKLGQGFQGTTFCTRRASGKGFACKSIKPKLLCKEDYEDVRE 61
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Qy 60 VTINSTLPEHNPVVKLKYATYEDNETVHLVLMELCEGGEFGRIIVARGHYTERAAATVARTI 119
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Qy 120 AEVVRMCHVNGVHRDLKPNFLFANKKENSALKKAIDFGLSVLPKPGERFTEIVGSPYYM 179
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Db 122 VEVVEACHSLGVHRDLKPNFLFDITDEDAKLKATDFGLSVFYKPGESFCDDVVGSPYYV 181
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Qy 180 APEVLKRNYPEDVMSAGVILYLLCGVPPFWAETEOGVVALAILRGVLDPKRDPWQSIS 239
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Qy 240 ESAKSLVKQMLEPDPSTKRLTAQOVLDPHPI 269
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Db 242 DSAKDLIRKMLDQNPKTRLTAEVLRHPWI 271
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RESULT 15
US-09-547-422-25
; Sequence 0, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: /note= "protein sequence for
; soybean CDPK as shown in Figure 34."
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
;
; US-09-547-422-25
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Query Match      60.7%; Score 861.5; DB 3; Length 463;
Best Local Similarity 61.5%; Pred. No. 4.5e-80;
Matches 166; Conservative 36; Mismatches 67; Indels 1; Gaps 1;

QY      1  MANQTQ-ISKYILGRELGRGEGITYLCTDRETREALACKSISKRLRTAVDVEDVRR 59
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      2  LPQRTQNIREVYEVGRKLGQGGQTTFECTRRASGGKFAKSPKRLCKEDYEDVWRE 61
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      60  VTIMSTLPEHPNVVYKLNKATYEDNETVHLMELCEGGELFGRIVARGHYTERAAATVARTI 119
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QY      62  IQIMHLSHANVVRTEGTEDSTAVHLMELCEGGELFDRIYQGHYSERQARLIKTI 121
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      120  AEVVRMCHVNGVMHRDLKPNFLFANKKENSALKATDFGLSVLFKPGERFETIVGSPYYM 179
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      122  VEVVEACHSLGVMHRDLKPNFLFDITDEDAKLKATDFGLSVFYKPGESPCDVVGSFYV 181
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QY      180  APEVLKRNYPGVVDVNSAGVILILLCGVPPFWAETEOGVVALAILRGVLDPKRDPWSQIS 239
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      182  APEVLRLKLYGPESDVNSAGVILYLSGVPPFWAESPPGIFRQILLGLKLDHFSEPMPSIS 241
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      240  ESAKSLVKQMLEPDSKRLTAQOVLDPWI 269
Db      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      242  DSAKDLIRKMLDQNPKRLTAHEVLRHPWI 271
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; Search completed: October 14, 2005, 10:54:49
; Job time : 22 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 14, 2005, 17:14:28 ; Search time 4656 Seconds
(without alignments)
2851.531 Million cell updates/sec

Title: US-08-989-881-2
Perfect score: 1419
Sequence: 1 MANQKISDKYLGRG.....TKRLTAQVLDHPWQNAKK 274

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Delop 6.0			7.0

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Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :

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14: gb.vi.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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VERSION	9	1186	83.6	2313	8	F25A4
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	21	1135	80.0	2086	8	AY062539
	22	1135	80.0	2087	6	AX077698
	23	1135	80.0	2162	6	AX077694
	24	1133	79.8	2166	8	AK068315
	25	1132	79.8	1770	6	AX553371
	26	1127	79.4	1602	6	AX507609
	27	1127	79.4	1726	6	AX077695
	28	1127	79.4	1896	6	ATU20624
	29	1124	79.2	1868	6	AX927170
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	32	1115	78.6	2252	8	AK066615
	33	1106	77.9	2127	8	AK101942
	34	1094	77.1	2163	8	AK105102
	35	1041	73.4	2390	8	AK072981
	36	1030	72.6	2216	8	AK117892
	37	1027	72.4	1892	6	AX537776
	38	1011.5	71.3	1818	6	AX531774
	39	997	70.3	90020	8	ATT24H18
	40	997	70.3	98506	8	ATT2L20
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ALIGNMENTS

RESULT 1
ATU73610
LOCUS
DEFINITION Arabidopsis thaliana ATCDPK1a (cpk1a) mRNA, partial cds.
ACCESSION U73610
VERSION U73610.1
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
REFERENCE 1 (bases 1 to 822)
AUTHORS Sheen, J.
TITLE Ca2+-dependent protein kinases and stress signal transduction in plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 822)
AUTHORS Sheen, J.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1996) Department of Molecular Biology, Massachusetts General Hospital, 50 Blossom Street, Boston, MA 02114, USA

Location/Qualifiers
1. 822
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DFKQPMQSISSAKSLVKOMLEPDSFKELTAQOVLDPHWNQAKKAPNGLDVRK
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ORIGIN

Alignment Scores: 8.1e-132 Length: 1626
 Pred. No.: 1395.00 Matches: 269
 Score: 1395.00
 Percent Similarity: 99.27% Conservative: 3
 Best Local Similarity: 98.18% Mismatches: 2
 Query Match: 98.31% Indels: 0
 DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x BT008900 (1-1626)

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Qy 21 GluPheGlyIleThrTyrLeuGlySerThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Dy 205 GAATTCGGAATCACGTATCTTTGTACAGATAGAGAGACTCGTGAAGCTTTAGCTGCAAA 264
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Dy 265 TCAATCTCCAGAGAAAGCTCCGAACCGCGTCGATGCGAAGACGTCGTCGTGAAGTC 324
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Qy 81 AspAsnGluThrValHisLeuValMetGluLeuGlyGlyGlyGluLeuPheGlyArg 100
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Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAen 140
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Qy 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGlu 240
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LOCUS AY140016 2044 bp mRNA linear PLN 02-SEP-2002
DEFINITION Arabidopsis thaliana calcium-dependent protein kinase, putative
            (Atlg74740) mRNA, complete cds.
ACCESSION AY140016 GI:22655134
VERSION AY140016.1
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 2044)
AUTHORS Tripp,M., Southwick,A., Karlin-Neumann,G., Nguyen,M., Miranda,M.,
            Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
            Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
            Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
            Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
            Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
DIRECT SUBMISSION
SUBMITTED (12-AUG-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
e-mail for correspondence: arab@sequence.stanford.edu
COMMENT
            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.
            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Tripp,M.,
            Southwick,A., Nguyen,M., Palm,C.J., Jones,T., Wu,T., Chen,H.,
            Cheuk,R., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
            Lee,J.M., Kim,C.J., Quach,H.L., Shinn,P., Tang,C.C., Toroumi,M.,
            Wallender,E.K., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S.,
            Ecker,J., Theologis,A. and Davis,R.W.
            Tripp,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally
            to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
            (SSP/Stanford) contributed equally to this work as PIs.
FEATURES
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ORIGIN

Alignment Scores:

Pred. No.: 1.08e-131 Length: 2044
Score: 1395.00 Matches: 269
Percent Similarity: 99.27% Conservative: 3
Best Local Similarity: 98.18% Mismatches: 2
Query Match: 98.31% Indels: 0
DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x AY140016 (1-2044)

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Qy 21 GluPheGlyIleThrTyrLeuGlyThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 373 GAATTCGGAATCACGTATCTTTGACAGATAGAGAGACTCGTGAAGCTTTAGCTTGCAA 432
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgArgGluVal 60
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Db 553 GATAACGAGAAAGCTGATCTTGTGATGAGCTTTGTGAAGGAGGTGAGCTTTTGTATCGG 612
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RESULT 4
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LOCUS Sequence 1859 from Patent WO0216655.
DEFINITION AX507164
ACCESSION AX507164
VERSION AX507164.1 GI:23388401
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1
AUTHORS Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL Patent: WO 0216655-A 1859 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH) Location/Qualifiers
source 1.1638
/organism="Arabidopsis thaliana"
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ORIGIN

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Score: 1322.00 Matches: 253
Percent Similarity: 95.26% Conservative: 8
Best Local Similarity: 92.34% Mismatches: 13
Query Match: 93.16% Indels: 0
DB: 6 Gaps: 0
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Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgArgGluVal 60
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Qy 81 AspAenGluThrValHisLeuValMetGluLeuGlyGlyGlyGlyGlyGlyArg 100
Db 397 GATAACGAGAAAGCTGCTGCTGTTATGAGCTTTGTGAAGGAGGTGAGCTTTTGTATCGG 456
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Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAen 140
Db 517 GAGGTGTGATGATGTCTACTCTTAATGGAGTTATGTCATCGAGTTTGAACCTGAGAA 576
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Qy 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
Db 637 GTGTTCTTCAACCTGGAGATAAGTTTACAGAGATTTAGAGAAATGCTCGTATTATATGCT 696
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Db      877  AGTGCAAGAGCTTGTGAGCAGATGTTGGATCTCTGATCCGACTTAAGCGGTAACTGCT 936
Qy      261  GlnGlnValLeuAspHisProTrpIleGlnAsnAlaLysLys 274
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LOCUS      AX651704      1638 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION Sequence 533 from Patent WO03000898.
ACCESSION  AX651704
VERSION     AX651704.1  GI:29154522
KEYWORDS   Arabidopsis thaliana (thale cress)
SOURCE     Arabidopsis thaliana
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
REFERENCE  Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
AUTHORS    Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
TITLE      Plant genes involved in defense against pathogens
JOURNAL    Patent: WO 03000898-A 533 03-JAN-2003;
SYNOPSIS   Syngenta Participations AG (CH)
FEATURES   Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.:      2.13e-124      Length:      1638
Score:          1322.00      Matches:     253
Percent Similarity: 95.26%      Conservative: 8
Best Local Similarity: 92.34%      Mismatches: 13
Query Match:     93.16%      Indels:      0
DB:              6              Gaps:        0

US-08-989-881-2 (1-274) x AX651704 (1-1638)

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Qy      21  GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db      217  GAATTCGGAATCACTTACCTCTGTACTGATCGTGAACCCAGCAGCTTGTAGCTTGCAAA 276
Qy      41  SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
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Qy      61  ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db      337  GCGATTATGCTACTTTTACCTGAGCATCCAAACGTTAGTTAAGCTTAGTTATGAG 396
Qy      81  AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyLeuPheGlyArg 100
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Qy      141  PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
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Qy      161  ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
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Qy      261  GlnGlnValLeuAspHisProTrpIleGlnAsnAlaLysLys 274
Db      937  CAGCAAGTGTAGCTCACCATCGATACAGATGCAAGATGCAAGAAA 978

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BT004566
LOCUS      Arabidopsis thaliana At1g18890 gene, complete cds.
DEFINITION
ACCESSION  BT004566
VERSION     BT004566.1  GI:28416562
KEYWORDS   FLI, CDNA.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1638)
Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P.,
Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
Ecker, J.R.
Arabidopsis ORF clones
Unpublished
2 (bases 1 to 1638)
Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P.,
Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
Ecker, J.R.
Direct Submission
Submitted (19-FEB-2003) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,

```

USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C. J., Shinn, P., Bowser, L., Chan, M. M., Chang, C. M., Dale, J. M., Hsuan, V. W., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J. M., Lin, J., Miranda, M., Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H. L., Southwick, A., Tang, C. C., Toriumi, M., Wong, C., Wu, H. C., Yamada, K., Yu, G., Yuan, S., Davis, R. W., Theologis, A., and Ecker, J. R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J. R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers
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ORIGIN
Alignment Scores:
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Score: 1318.00 Matches: 252
Percent Similarity: 94.89% Conservative: 8
Best Local Similarity: 91.97% Mismatches: 14
Query Match: 92.88% Indels: 0
DB: Gaps: 0

US-08-989-881-2 (1-274) x BT004566 (1-1638)

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Db 277 TCGATTTCAAAGCGAAGACTTCGACAGCTGCTGATATCGAAGACGTTCTGCTGAGGTA 336
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RESULT 7
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DEFINITION (CDPK), complete cds.
ACCESSION D21805.1 GI:1235716
VERSION D21805
KEYWORDS calcium-dependent protein kinase; ATCDPK1.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 1842)
AUTHORS Urao, T., Katagiri, T., Mizoguchi, T., Yamaguchi-Shinozaki, K.,
Hayashida, N. and Shinozaki, K.
TITLE Two genes that encode Ca(2+)-dependent protein kinases are induced
by drought and high-salt stresses in Arabidopsis thaliana
JOURNAL Mol. Gen. Genet. 244 (4), 331-340 (1994)
MEDLINE 94359455
PUBMED 8078458
REFERENCE 2 (bases 1 to 1842)
AUTHORS Shinozaki, K.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1993) Kazuo Shinozaki, Tsukuba Life Science
Center, The Inst. of Physical and Chemical Res.: 3-1-1 Kohyodai,
Tsukuba, Ibaraki 350, Japan (E-mail: shinozaki@riken.go.jp,
Tel: 0298-36-4359, Fax: 0298-36-9060)
COMMENT On Mar 22, 1996 this sequence version replaced gi:540481.
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ORIGIN

Alignment Scores:

Pred. No.: 6.29e-124 Length: 1842

Score: 1318.00 Matches: 252

Percent Similarity: 94.89% Conservative: 8

Best Local Similarity: 94.97% Mismatches: 14

Query Match: 92.88% Indels: 0

DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x ATHCDPKA (1-1842)

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Qy 21 GluPheGlyIleThrTyrLeuGlyThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 191 GAATTCGGAAATCACTTACTCTGTACTGATCGTGAACCCAGAGCTTAGCTTGCCTCAA 250
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Db 491 GAGGTTGTGATGATGTGTCACCTCTAATGAGGTTATGTCATCGAGTTTGAACCTGAGAT 550
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DEFINITION Arabidopsis thaliana chromosome 1 BAC F25A4 sequence, complete
ACCESSION AC008263
VERSION AC008263.2 GI:5868932
KEYWORDS HTG.
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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
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Vysotskaia, V.S., Schwartz, J.R., Yu, G., Toriumi, M., Lenz, C., Liu, S.,
Lee, J.M., Li, J., Gonzalez, A., Liu, A., Liu, K., Vaysberg, M.,
Sakano, H., Chin, C., Choi, E., Chio, J., Altafi, H., Araujo, R.,
Brooks, S., Buehler, E., Chao, Q., Conn, D., Conway, A.B., Dunn, P.,
Hansen, N., Hwang, B., Huizar, L., Khan, S., Kim, C., Palm, C.,
Rowley, D., Shinn, P., Walker, M., Davis, R.W., Ecker, J.R.,
Federspiel, N.A. and Theologis, A.
Arabidopsis thaliana chromosome 1 BAC F25A4 sequence
Unpublished
2 (bases 1 to 115721)
Theologis, A.
Direct Submission
Submitted (31-JUL-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 115721)
Theologis, A.
Direct Submission
Submitted (10-SEP-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 115721)
Theologis, A.
Direct Submission
Submitted (15-SEP-1999) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
On Sep 10, 1999 this sequence version replaced gi:5668776.
The sequence of BAC F25A4 from Arabidopsis thaliana chromosome 1.
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US-08-989-881-2 (1-274) x F25A4 (1-115721)

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QY	165	-----	165
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QY	166	-----GlyGluArgPhe	169
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QY	210	ProPheTyrAla-----	213
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RESULT 9

AF276999

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

mRNA

CDS

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

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88.56%

Length:

Matches:

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18

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US-08-989-881-2 (1-274) x AF276999 (1-2313)

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complete sequence.
ACCESSION AC011809
VERSION AC011809.2 GI:6579253
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ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 108767)
Fedeerspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altati,H., Araujo,R., Rowley,D., Buehler,E., Dunn,P., Chin,C., Chlou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
Unpublished
2 (bases 1 to 108767)
Fedeerspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altati,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E., Chin,C., Chlou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsy,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Theologis,A., Toriumi,M., Vayaberg,M., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (15-OCT-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
3 (bases 1 to 108767)
Fedeerspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altati,H., Araujo,R., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (15-DEC-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
4 (bases 1 to 108767)
Fedeerspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altati,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (22-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
On Dec 15, 1999 this sequence version replaced gi:6041764.
e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are described as 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/~chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
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US-08-989-881-2 (1-274) x AC011809 (1-108767)

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ACCESSION CO803946
VERSION CO803946.1 GI:47110607
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ORGANISM Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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REFERENCE
1 Inze, D., de Veylder, L. and Vlieghe, K.
AUTHORS
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TITLE Identification of novel e2f target genes and use thereof
JOURNAL Patent: WO 2004035798-A 357 29-APR-2004;
CropDesign N.V. (BE)
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Query Match: 81.82% Indels: 0
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US-08-989-881-2 (1-274) x CO803946 (1-1617)
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Db 652 GCGCAGAGGTTTAAACGAAATCGTTGTTAGTCCGCTACTACATGCTCCGAGGTCCTAAAA 711
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Qy 206 CysGlyValProPheThrPalaGluThrGluGlnGlyValAlaLeuAlaIleLeuArg 225
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Qy 226 GlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeu 245
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Qy 246 ValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAsp 265
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Db          952 CACCCGTGGTTACAGAAATGCAAG 975
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DEFINITION Arabidopsis thaliana At3g57530 gene, complete cds.
ACCESSION  BT012274
VERSION     BT012274.1  GI:45773913
KEYWORDS   FLI CDNA.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 1617)
AUTHORS    Cheuk,R., Chen,H., Kim,C.J., Shinn,P. and Ecker,J.R.
TITLE      Arabidopsis ORF clones
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1617)
AUTHORS    Cheuk,R., Chen,H., Kim,C.J., Shinn,P. and Ecker,J.R.
TITLE      Direct Submission
JOURNAL    Submitted (27-MAR-2004) Salk Institute Genomic Analysis Laboratory
            (SIGNAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
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ORIGIN
Alignment Scores:
Pred. No.:      4,766-108      Length:      1617
Score:          1161.00      Matches:      213
Percent Similarity: 88.43%      Conservative: 24
Best Local Similarity: 79.48%      Mismatches:  31
Query Match:    81.82%      Indels:      0
DB:             8      Gaps:      0
US-08-989-881-2 (1-274) x BT012274 (1-1617)
Qy          6 GlnileSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThr 25
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Db          172 GAGATCGAGTCTAAATACACGTTGGGAGAGAGCTAGCTCGTGGAGAAATTCGTTGTACG 231
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Qy          26 TyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArg 45
           ...
Db          232 TATCTATGCTACTGATGATGAGGACACGACGCTTTTGGTTGTAATTCGATTTGAAGAAG 291
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Qy          46 LysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThr 65
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DEFINITION Arabidopsis thaliana At3g57530 mRNA, complete cds.
ACCESSION  BT011630
VERSION     BT011630.1  GI:44681391
KEYWORDS   FLI CDNA.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 1700)
AUTHORS    Kim,C.J., Chen,H., Cheuk,R., Shinn,P. and Ecker,J.R.
TITLE      Arabidopsis cDNA clones
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1700)
AUTHORS    Kim,C.J., Chen,H., Cheuk,R., Shinn,P. and Ecker,J.R.
TITLE      Direct Submission
JOURNAL    Submitted (28-FEB-2004) Salk Institute Genomic Analysis Laboratory
            (SIGNAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
FEATURES   Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 5,078-108 Length: 1700
Score: 1161.00 Matches: 213
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Best Local Similarity: 79.48% Mismatches: 31
Query Match: 81.82% Indels: 0
DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x BT011630 (1-1700)

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Db 226 GAGATCGAGTCTAAATACACGTTGGGAGAGAGCTAGTCTGGAGAAATTCGTTCTAGC 285
Qy 26 TyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLeuSerIleSerIle 45
Db 286 TATCTATGTACTGATAAGGAGACACGACGCTTTTGTCTGTAATTCGATTTGAAGAAG 345
Qy 46 LysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThr 65
Db 346 AAGCTGAGACAGCTGTTGATATTCAGATGTTAGGAGAGGTTGAGATTTAGGAGAT 405
Qy 66 LeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrVal 85
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RESULT 14
AX077712
LOCUS AX077712 1967 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 19 from Patent WO0107592.
ACCESSION AX077712
VERSION AX077712.1 GI:13122087
KEYWORDS
SOURCE Fragaria x ananassa
ORGANISM Fragaria x ananassa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
REFERENCE 1
AUTHORS Holt, C.D., White, A.J., Michael, A.J. and Osborn, R.W.
TITLE Herbicide resistant plants and methods for the production thereof
JOURNAL Patent: WO 0107592-A 19 01-FEB-2001;
ZENECA LIMITED (GB)
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Pred. No.: 1,238-107 Length: 1967
Score: 1158.00 Matches: 215
Percent Similarity: 88.89% Conservative: 25
Best Local Similarity: 79.63% Mismatches: 30
Query Match: 81.61% Indels: 0
DB: 6 Gaps: 0

US-08-989-881-2 (1-274) x AX077712 (1-1967)

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Qy 25 ThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLys 44
Db 223 ACGTATCTGTGTTACTGACAGGCCACCAACGAGAACTACGCTTGCAAAATCGATATCGAAG 282
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Db 283 CAGAACTGAGGACGCTGTGGATATTGAAGATGTGAGGAGGGAAGTTGAGATCATGAAG 342
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QY 125 MetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAla 144
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 QY 205 LeuCysGlyValProProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaileLeu 224
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RESULT 15

AF035944

LOCUS

DEFINITION Fragaria x ananassa calcium-dependent protein kinase (MAX17) mRNA, complete cds.

ACCESSION AF035944

VERSION AF035944.1 GI:2665889

KEYWORDS

SOURCE Fragaria x ananassa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria;

1 (bases 1 to 1967)

Llop-Tous, I., Dominguez-Puigjaner, E. and Vendrell, M.

Direct Submission

Submitted (26-NOV-1997) Agrobiologia, CSIC, Jordi Girona 18-26,

Barcelona 08034, Spain

FEATURES

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polyA_site

ORIGIN

Alignment Scores:

Pred. No.: 1-236-107 Length: 1967

Score: 1158.00 Matches: 215

Percent Similarity: 88.89% Conservative: 25

Best Local Similarity: 79.63% Mismatches: 30

Query Match: 81.61% Indels: 0

DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x AF035944 (1-1967)

QY 5 ThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIle 24
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 QY 25 ThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLys 44
 Db 223 ACGTATCTGTGTACTGACAAAGGCCCAACGAGAACTACGCTTGCATAATCGATATCGAAG 282
 QY 45 ArgLysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSer 64
 Db 283 CAGAAACTGAGACGCGCTGTGATATTGAAGATGTGAGAGGGAAGTTGAGATCATGAAG 342
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 Db 643 CTGTGTGAAGATTTCAGTGAATTTGTTGGAAGTCCATCTACTACTGCTCTCGAGTGCTA 702
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Total number of hits satisfying chosen parameters: 8780412

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Maximum Match 100%
Listing first 45 summaries

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11: Geneseqn2003ds:
12: Geneseqn2004as:
13: Geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1419	100.0	1020	2 AAV36878	AAV36878 Nucleotid
2	1419	100.0	1020	4 AAL66819	AAL66819 ATCDPK1a
3	1322	93.2	1638	6 ABZ14054	ABZ14054 Arabidops
4	1322	93.2	1638	8 ADA68553	ADA68553 Arabidops
5	1161	81.8	1617	12 ADN72462	Adn72462 Thale cre

6	1161	81.8	1836	3 AAC47633	AAC47633 Arabidops
7	1158	81.6	1967	4 AAF74280	AAF74280 Strawberry
8	1135	80.0	2087	4 AAF74266	AAF74266 Arabidops
9	1135	80.0	2162	4 AAF74262	AAF74262 Arabidops
10	1132	79.8	1770	8 ADA69918	ADA69918 Rice gene
11	1132	79.8	1770	12 ADJ39574	ADJ39574 Plant cDN
12	1127	79.4	1602	6 ABZ14499	ABZ14499 Arabidops
13	1127	79.4	1726	4 AAF74263	AAF74263 Arabidops
14	1124	79.2	1868	10 ADF38032	ADF38032 Synchroni
15	1115	78.6	1515	8 ADA70638	ADA70638 Rice gene
16	1071	75.5	960	12 ADA44509	ADA44509 Plant cDN
17	1027	72.4	1692	8 ADA70323	ADA70323 Rice gene
18	1011.5	71.3	1818	8 ADA69721	ADA69721 Rice gene
19	970	68.4	912	12 ADJ42517	ADJ42517 Plant cDN
20	957	67.4	1647	4 AAF74281	AAF74281 Liverwort
21	957	67.4	1647	4 AAF74282	AAF74282 Liverwort
22	947	66.7	2230	6 ABA91081	ABA91081 Physcomit
23	930	65.5	690	10 ADC08881	ADC08881 Corn DNA
24	930	65.5	690	12 ADJ44765	ADJ44765 Plant cDN
25	930	65.5	1797	8 ADA71210	ADA71210 Rice gene
26	929	65.5	1392	3 AAC48741	AAC48741 Arabidops
27	921	64.9	1473	12 ADJ44645	ADJ44645 Plant cDN
28	916	64.6	1833	6 ABZ14529	ABZ14529 Arabidops
29	916	64.6	1839	8 ADA71195	ADA71195 Rice gene
30	907	63.9	1719	8 ADA70078	ADA70078 Rice gene
31	903	63.6	3054	3 AAC45753	AAC45753 Arabidops
32	900	63.4	1133	4 AAC85833	AAC85833 Tobacco h
33	899	63.4	2550	4 AAF74283	AAF74283 Cucurbita
34	898	63.3	2439	8 ADA70481	ADA70481 Rice gene
35	895	63.1	1795	12 ADJ39906	ADJ39906 Plant cDN
36	894	63.0	2022	4 AAF74285	AAF74285 Vigna rad
37	893	62.9	2040	4 AAF74278	AAF74278 Rice calc
38	891	62.8	1782	8 ADA71107	ADA71107 Rice gene
39	890	62.7	2363	4 AAF74284	AAF74284 Common ic
40	887.5	62.5	1473	6 ABZ12981	ABZ12981 Arabidops
41	887	62.5	1488	6 ABZ12899	ABZ12899 Arabidops
42	887	62.5	1747	6 ABA06021	ABA06021 Arabidops
43	887	62.5	1761	3 AAC42353	AAC42353 Arabidops
44	887	62.5	2306	4 AAF74272	AAF74272 Maize cal
45	884	62.3	1650	12 ADI45326	ADI45326 Rice isop

ALIGNMENTS

RESULT 1
AAV36878
ID AAV36878 standard; cDNA; 1020 BP.
XX AAV36878;
AC AAV36878;
XX 27-AUG-2003 (revised)
DT 12-OCT-1998 (first entry)
XX Nucleotide sequence of ATCDPK1a PK domain.

ATCDPK1a; protein kinase; PK; tolerance; drought; salinity; cold; heat;
fruit; ornamental; vegetable; cereal; field crops; db.

Arabidopsis sp.

XX Key Location/Qualifiers
XX CDS 97..918
FT /*tag= a
FT /product= "ATCDPK1a PK protein"
FT /note= "no stop codon specified"

XX PN WO9826045-A1.

XX PD 18-JUN-1998.

XX PF 12-DEC-1997; 97WO-US023019.

XX PR 13-DEC-1996; 96US-0032966P.

XX (GEHO) GEN HOSPITAL CORP.
 PA Sheen J;
 XX WPI; 1998-348509/30.
 DR P-PSDB; AAW49837.
 XX
 PT Protecting plants against environmental stress - by introducing protein
 PT kinase domain-containing gene, calcium dependent protein kinase gene or
 PT calcium/calmodulin-dependent gene.
 XX
 PS Claim 17; Fig 5; 62pp; English.
 XX
 CC This is the nucleotide sequence of the ATCDPK1a protein kinase (PK)
 CC domain isolated from the Arabidopsis cDNA library, and used in the method
 CC of the invention to protect plants against environmental stress. The
 CC methods can be used for improving the tolerance of plants to
 CC environmental stresses such as drought, salinity, cold and heat. They
 CC provide for increased production efficiency, as well as for improvements
 CC in quality and the yield of crop plants and ornamentals. The methods
 CC contribute to the production of high quality and high yield agricultural
 CC products, e.g. fruits, ornamentals, vegetables, cereals, and field crops.
 CC (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 1020 BP; 265 A; 194 C; 280 G; 277 T; 0 U; 4 Other;

Alignment Scores:
 Pred. No.: 4,35e-155 Length: 1020
 Score: 1419.00 Matches: 274
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-08-989-881-2 (1-274) x AAV36878 (1-1020)

Qy 1 MetAlaasnGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20
 Db 97 ATGGCTAATCAAACTCAGATCAGCGACAACTATCTTAGGACGAGAACTCGGTGCGGC 156
 Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
 Db 157 GAATTCGGATACGATATCTTTGTACAGATAGAGAGACTCGTAGGCTTTAGCTTGCAA 216
 Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
 Db 217 TCAATCTCCAAGAGAAAGCTCCGAACCGCGTCGATGTGGAAGACGTCCTCGTGAAGTC 276
 Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
 Db 277 ACGATCATGTCAACTTTACCGGAACACCCCAACGTTGTGAACCTTAAAGCGACTTTATGAG 336
 Qy 81 AspAsnGluThrValHisLeuValMetMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
 Db 337 GATAACGAGACCGTGATCTTTGTGATGAGCTTTGTGAGGAGGTGAGCTTTTGTGTCGG 396
 Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAla 120
 Db 397 ATTGTTGCAAGAGAGACATTATACAGAGCGTCGCGCGCTACCGTCGCGAAGCATCGCG 456
 Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
 Db 457 GAATTTGTGAGGATGTCTATGTCATGTCTCAATGGTTATGATGATAGATTTGAAGCTTGAGAT 516
 Qy 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
 Db 517 TTCTTGTTTCTTAAAGAAGAGAGAAATTCGCACCTTAAGGCTATTGATTTGGTTTATCT 576
 Qy 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
 Db 577 GTTCTCTTTAAACCTGGAGAGAGGTTTACAGAGATTTGTGGAAGTCTCTATTATATGGCT 636

Qy 181 ProGluValLeuLysArgSerTyrGlyProGluValAspValTrpSerAlaGlyValIle 200
 Db 637 CCAGAAAGTGTGAAGAGAAATATGACCCAGAGGTTGATGTGTGGAGTCTGCTGGAGTTATC 696
 Qy 201 LeuTyrIleLeuLeuCysGlyValProProPheTtpAlaGluThrGluGlnGlyValAla 220
 Db 697 CTCTACATCTTCTTTGTGGTGTCTCTCGCTTTTGGGCAGAGACTGCAACAAGGTGTGGCT 756
 Qy 221 LeuAlaIleLeuArgGlyValLeuLeuAspPheLysArgAspProTrpSerGlnIleSerGlu 240
 Db 757 CTTGCCATCTTGAAGGAGTCTTCTGATTTTAAAGAGAGATCCTTGGTCCGAGATATCAGAG 816
 Qy 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
 Db 817 AGCGCAAGAGCGCTTGTGAAGCAGATGTTGGAACTGATTCACCTAAGCGTTTGAAGTCT 876
 Qy 261 GlnGlnValLeuAspHisProTrpIleGlnAsnAlaLysLys 274
 Db 877 CAGCAAGTCTTGTGATCACCCTTGGATACAGATGCAAGTCAAGTCAAGCTTGAAGTCT 918

RESULT 2
 AAI66819
 ID AAI66819 standard; DNA; 1020 BP.
 XX
 AC AAI66819;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 DE ATCDPK1a PK domain nucleotide sequence.
 XX
 KW Plant protoplast; gene expression; Arabidopsis; PK; CDPK; ATCDPK1a;
 KW calcium activated protein kinase; calcium dependant protein kinase; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT CDS 97..918
 FT /*tag= a
 XX
 PN WO200168920-A1.
 XX
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001WO-US007999.
 XX
 PR 13-MAR-2000; 2000US-0189074P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Sheen J;
 XX
 XX WPI; 2001-611395/70.
 DR P-PSDB; AAG65759.
 XX
 PT Using plant protoplast expression systems for rapidly screening libraries
 PT of nucleic acids to identify gene that modulate expression of target
 PT genes.
 XX
 XX Example; Fig 5A-C; 95pp; English.
 PS
 CC The invention provides a high through-put assay for rapidly screening a
 CC library of nucleic acid molecules to identify a gene product that
 CC modulates expression of a gene of interest in plant protoplasts. The
 CC method comprises: (1) introducing into 1 or more plant protoplasts: (a) a
 CC reporter gene construct operably linked to a promoter of a gene of
 CC interest; and (b) a member of a library of nucleic acid molecules (the
 CC library member is expressed in the plant protoplasts); and (2) screening
 CC the protoplasts to determine whether the amount of gene expression of the
 CC reporter gene construct changes in response to the expression of the
 CC library members, a change in gene expression of the reporter gene
 CC construct identifying the gene product expressed by the library member as
 CC 1 that modulates expression of the gene of interest. The present sequence
 CC represents the nucleotide sequence of Arabidopsis calcium dependant

CC protein kinase (CDPK) ATCDPK1a PK domain
XX Sequence 1020 BP; 265 A; 194 C; 280 G; 277 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 4,35e-155 Length: 1020
Score: 1419.00 Matches: 274
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-08-989-881-2 (1-274) x AAI66819 (1-1020)

Qy 1 MetAlaenGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20
Db 97 ATGGCTATCAAACTCAGATCAGCGACAAAGTACATCTTAGGACGAGAACTCGGTGCGGCG 156
Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 157 GAATTCGGAAATCAGGTATCTTTGTACAGATAGAGACTCGTGAAGCTTTAGCTTGCANA 216
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Db 217 TCAATCTCCAAGAGAAAGCTCCGAACCGCGTCGATGTGGAAGAGCTCGTGGTGAAGTC 276
Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db 277 ACGATCATGTCAACTTTACCGGAACACCCAAACGTTGTGAAACTTTAAAGCGACTTATGAG 336
Qy 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
Db 337 GATTAACGAGACCGTGCATCTTGTGATGAGCTTTGTGAAGGAGGTGAGCTTTTGGTGGG 396
Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaIleThrValAlaArgThrIleAla 120
Db 397 ATTGTGCAAGAGGACATTATACAGAGCGTGGCGGCTACCGTCGCGAGAACGATCGCG 456
Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
Db 457 GAAGTGTGTGAGGATGTGTCATGTCAATGCTGTATGTCATAGAGATTTGAAGCCTGAGAA 516
Qy 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
Db 517 TTCCTGTTTGTCTAACAGAGAGAAATTCGCACTTAAGGCTATTGATTTTGGTTTATCT 576
Qy 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
Db 577 GTTCTCTTTAAACCTGGAGAGAGGTTTACAGAGATTGTTGAAGTCTTATTATATGCT 636
Qy 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
Db 637 CCAGAAGTGTGTTGAAGAGAAATATGACAGAGGTGATGTGTGGAGTGCTGGAGTTATC 696
Qy 201 LeuTyrIleLeuLeuCysGlyValProPheThrPAlaGluThrGluGlnGlyValAla 220
Db 697 CTCTACATCTTCTTTGTGGTGTCTCTCCGTTTGGCGAGAGACTGAACAAGGTGTGCT 756
Qy 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGlu 240
Db 757 CTTCGCCATCTTGAGGGAGTCTTGTGATTTTAAGAGAGATCCTTGTGTCAGATATCAGAG 816
Qy 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
Db 817 AGCCGAAGAGCCCTTGTGAAGCAGATGTTGAACCTGATTCACACTAAGCGTTTGAAGTCT 876
Qy 261 GlnGlnValLeuAspHisProTyrIleGlnAsnAlaLysLys 274
Db 877 CAGCAAGTCTTGTATCACCCTTGGATACAGAAATGCNAAGAAA 918

RESULT 3
ABZ14054
ID ABZ14054 standard; DNA; 1638 BP.

XX ABZ14054;
XX 21-JAN-2003 (first entry)
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 1859.
XX Arabidopsis thaliana; plant; gene; stress; transgenic; da.
XX Arabidopsis thaliana.
XX WO200216655-A2.
XX 28-FEB-2002.
XX 24-AUG-2001; 2001WO-US026685.
XX 24-AUG-2000; 2000US-0227866P.
XX 26-JAN-2001; 2001US-0264647P.
XX 22-JUN-2001; 2001US-0300111P.
XX (SCRI) SCRIPPS RES INST.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Harper JF, Krebs J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX Identifying a stress condition to which a plant cell has been exposed and
XX producing plants with increased tolerance to these abiotic stresses.
XX Claim 144; SEQ ID NO 1859; 577bp + Sequence Listing; English.
XX The invention relates to identifying a stress condition to which a plant
XX cell has been exposed, comprising: (a) contacting nucleic acid
XX representative of expressed polynucleotides in the plant cell with an
XX array or probes representative of the plant cell genome; and (b)
XX detecting a profile of expressed polynucleotides in the plant cell
XX characteristic of a stress response. The method is useful in the
XX production of transgenic plants, cells and seeds and in producing plants
XX with increased tolerance to abiotic stress. The present sequence is that
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
XX in methods of the invention. Note: The sequence data for this patent is
XX not represented in the printed specification but is based on sequence
XX information supplied to Derwent by the European Patent Office
XX SQ Sequence 1638 BP; 482 A; 291 C; 416 G; 449 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.67e-143 Length: 1638
Score: 1322.00 Matches: 253
Percent Similarity: 95.26% Conservative: 8
Best Local Similarity: 92.34% Mismatches: 13
Query Match: 93.16% Indels: 0
DB: 6 Gaps: 0

US-08-989-881-2 (1-274) x ABZ14054 (1-1638)

Qy 1 MetAlaenGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20
Db 157 ATGAGCAATCAAACTCAGATCAGCGACAAATACATCTTAGTCTCGTAATTAGTTCGAGGC 216
Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 217 GAATTCGGAAATCAGTCTTACCTCTGTACTGATCGTGAACCCACGAGCTTTAGCTTGCANA 276
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Db 277 TCGATTTCAAGCGAAAGCTTCGACAGCTTCGATATCGNAGACGTTCTGCTGAGGTA 336
Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db 337 GCGATTATGCTACTTTTACCTGAGACTCCAAACGACTTAAGCTTAAGGCTTAGTTATGAG 396

QY 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
 DB 397 GATAACGAGAACGTGCACTCTGGTTATGGAGCTTTGTGAAGGAGTGAGCTTTTGTATCGG 456
 QY 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
 DB 457 ATTGTTGCTAGAGACATTACAGGAGCTGCTGCTGACGCTGTTGCGAAGACGATTGCT 516
 QY 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuTyrProGluAsn 140
 DB 517 GAGGTTGTGATGATGTCATCTCTAATGGAGTTATGTCATCGAGATTGGAACCTGAGAAT 576
 QY 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaIleuLysAlaIleAspPheGlyLeuSer 160
 DB 577 TTCCTGTTGCTAATAAAGAGGAGAAATCTCCACTAAAGGCTATTGATTTGGCTGTCT 636
 QY 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
 DB 637 GTGTTCTTCAAACTGGAGATAAGTTTACAGAGATTGTAGAAAGTCCGTATTATATGGCT 696
 QY 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIle 200
 DB 697 CCAGAAAGTGTGAAGAGAGATTATGACACAGGCGTTGATGTGTGAGTGCCGAGTTATT 756
 QY 201 LeuTyrIleLeuLeuCysGlyValProPheTrpAlaGluThrGluGlnGlyValAla 220
 DB 757 ATCTATATCTTGTCTGTGTGTGTCTCTCGTTTGGGCTGAGACTGAACAAGGTGTGCT 816
 QY 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGlu 240
 DB 817 CTTCGATCTTGGGGGAGTCTTGATTTTAAAGAGACCTTGGCCTCAGATATCAGAG 876
 QY 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
 DB 877 AGTGCCAAAGAGCCTTGTGAAGCAGATGTTGATCCTGATCCGACTAAGCGTTAACTGCT 936
 QY 261 GlnGluValLeuAspHisProTyrIleGlnAsnAlaLysLys 274
 DB 937 CAGCAAGTGTAGCTCACCCATGGATACAGATGCAAGAA 978

RESULT 4

ADA68553

ID ADA68553 standard; DNA; 1638 BP.

AC ADA68553;

XX

XX 20-NOV-2003 (first entry)

XX Arabidopsis thaliana gene, SEQ ID 533.

XX Arabidopsis thaliana.

XX Plant; bacterial infection; fungal infection; viral infection; ds.

XX Arabidopsis thaliana.

XX WO2003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175250/17.

XX Identifying at least one gene involved in plant resistance or response to

XX pathogenic infection for conferring resistance or tolerance to a plant

XX bacterial, fungal or viral infection by determining or detecting plant

PT gene expression.

XX Claim 6; SEQ ID NO 533; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes

XX involved in plant resistance or response to pathogenic infection. M1

XX comprises identifying a gene whose expression is significantly altered in

XX the incompatible interaction of plant gene expression relative to

XX expression of the gene in an uninfected plant, in a mutant plant that

XX does not express a gene associated with response to pathogenic infection,

XX or in a corresponding incompatible or compatible interaction. (M1) is

XX useful for conferring resistance to resistance or tolerance to a plant to

XX bacterial, fungal or viral infection. The present sequence was used to

XX illustrate the invention.

XX Sequence 1638 BP; 482 A; 291 C; 416 G; 449 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 1-67e-143 Length: 1638

Score: 1322.00 Matches: 253

Percent Similarity: 95.26% Conservatives: 8

Best Local Similarity: 92.34% Mismatches: 13

Query Match: 93.16% Indels: 0

DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x ADA68553 (1-1638)

QY 1 MetAlaAsnGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20
 DB 157 ATGAGCAATCAAACTCAGATCAGCAGCAAAATACATCTTAGGTCGTGAATTAGGTCGAGGC 216
 QY 21 GluPheGlyIleThrTyrIleuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
 DB 217 GAATTCGGAATCACCTTACTCTGTACTGCTGAAACCCAGAGCTTTAGCTTGCAAA 276
 QY 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgArgGluVal 60
 DB 277 TCGATTTCCAAAGCGAAAGCTTCGAACAGCTGTCGATATCGAAGAGCTTCTGCTGAGGTA 336
 QY 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
 DB 337 GCGATTATGCTACTTTACCTGAGCATCCAAACGTAGTTAAGCTTAAGCTAGTTATGAG 396
 QY 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
 DB 397 GATAACGAGAACGTGCACTCTGGTTATGGAGCTTTGTGAAGGAGTGAGCTTTTGTATCGG 456
 QY 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
 DB 457 ATTGTTGCTAGAGACATTACAGGAGCGTGTCTGCTGACGCTGTTGCGAAGACGATTGCT 516
 QY 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
 DB 517 GAGGTTGTGATGATGTCATCTAATGGAGTTATGTCATCGAGATTGGAACCTGAGAAT 576
 QY 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
 DB 577 TTCCTGTTGCTAATAAAGAGGAGAAATCTCCACTAAAGGCTATTGATTTGGCTGTCT 636
 QY 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
 DB 637 GTGTTCTTCAAACTGGAGATAAGTTTACAGAGATTGTAGAAAGTCCGTATTATATGGCT 696
 QY 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIle 200
 DB 697 CCAGAAAGTGTGAAGAGAGATTATGACACAGGCGTTGATGTGTGAGTGCCGAGTTATT 756
 QY 201 LeuTyrIleLeuLeuCysGlyValProPheTrpAlaGluThrGluGlnGlyValAla 220
 DB 757 ATCTATATCTTGTCTGTGTGTGTCTCTCGTTTGGGCTGAGACTGAACAAGGTGTGCT 816
 QY 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGlu 240

Db 817 CTTCGATCTTGGCGGAGTCTTGATTTTAAGAGAGACCCTTGGCTCAGATATCAGAG 876
 Qy 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
 Db 877 AGTGCACAGAGCTTGTGAAGCAGATGTTGGATCTCGACATCCGAGCGTTAACTGCT 936

Qy 261 GlnGlnValLeuAspHisProTrpIleGlnAsnAlaLysLys 274

Db 937 CAGCAGGTGTTAGCTCACCATGGATACAGATGCAAGAA 978

RESULT 5

ADN72462
 ID ADN72462 standard; cDNA; 1617 BP.

XX AC ADN72462;

XX DT 15-JUL-2004 (first entry)

XX DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 357.

XX KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;

XX KW growth regulator; animal feed product; thale cress;

XX KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.

XX OS Arabidopsis thaliana.

XX PN WO2004035798-A2.

XX PD 29-APR-2004.

XX PF 20-OCT-2003; 2003WO-EP011658.

XX PR 18-OCT-2002; 2002EP-00079408.

XX PA (CROP-) CROPDESIGN NV.

XX PI Inze D, De Veylder L, Vlieghe K;

XX DR WPI; 2004-348466/32.

XX DR P-PSDB; ADN72463.

PT Altering plant characteristics, useful for producing plants for enzyme or
 PT pharmaceutical production comprises modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.

XX PS Claim 1; SEQ ID NO 357; 134pp; English.

XX CC This invention relates to a novel method for altering one or more plant
 CC characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 CC or physiology, altered endoreplication, biochemistry, signal
 CC transduction, storage lipid mobilisation and/or altered photosynthesis,
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a
 CC role in a variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polynucleotide sequence is thale cress cDNA
 CC upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa
 CC transcription factor, given in an exemplification of the invention.

XX SQ Sequence 1617 BP; 499 A; 271 C; 430 G; 417 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.16e-125 Length: 1617
 Score: 1161.00 Matches: 213

Percent Similarity: 88.43% Conservative: 24
 Best Local Similarity: 79.48% Mismatches: 31
 Query Match: 81.82% Indels: 0
 DB: 12 Gaps: 0

US-08-989-881-2 (1-274) x ADN72462 (1-1617)

Qy 6 GlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThr 25
 Db 172 GAGATCGAGTCTAAATACACGTTGGGGAGAGAGCTAGGTCTGGAGAAATTCGGTGTACG 231

Qy 26 TyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArg 45
 Db 232 TATCTATGTACTGATAAGGAGACAGACGCTTTTGTCTGTTAATCCATTTTGAGGAAG 291

Qy 46 LysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThr 65
 Db 292 AAGCTGAGGACAGCTGTTGATATTAGATCTTAGGAGAGAGGTTGAGATTATGAGGCAT 351

Qy 66 LeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrVal 85
 Db 352 ATGCTCAGCATCTCTAATGTTTGTACTTTTGAAGGAGACTTATGAGGATGAGCATCTGTT 411

Qy 86 HisLeuValMetGluLeuCysGluGlyGluLeuPheGlyArgIleValAlaArgGly 105
 Db 412 CATTTGGTTATGGAGCTTTGTGAAGGTGGTGAATTTGTGATAGATTGTTGCTAGAGGG 471

Qy 106 HisTyrThrGluArgAlaLeaAlaThrValAlaAlaArgThrIleAlaGluValValArgMet 125
 Db 472 CATTATACTGAGAGAGCTGCTGCTGTCTCACTAAGACCATCATGGAAGATTGTTCCAGGTG 531

Qy 126 CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
 Db 532 TGTCAATAGCATGGGGTAATGCACAGGGACCTGAAACCTGAGAACTCTCTGTTGGAAAC 591

Qy 146 LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro 165
 Db 592 AAGAAAGGAGACTGCACCTCTTAAAGCCATTGATTTGGTCTCTCTGTTCTTTAAACCA 651

Qy 166 GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys 185
 Db 652 GCGCAGAGGTTTAACGAAATCGTTGGTAGTCCGTACTACATGGCTCCGAGGTGCTAAAA 711

Qy 186 ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 205
 Db 712 CGGAATTTATGGTCCAGAAATGTGATATTGGAGTCAGGTGTAATTTCTTTACATACCTGTA 771

Qy 206 CysGlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArg 225
 Db 772 TGTGGTCTCCGCTTTCTGGCAGAACTGAACAGAGGTTGCACAGCAATTTATTTCGA 831

Qy 226 GlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeu 245
 Db 832 TCTGTACTAGACTTCAGAAAGGAGCCCATGCCCCAAGGTTTCTGAAAAACGCAAAAGACCTT 891

Qy 246 ValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAsp 265
 Db 892 ATCAGGAAAAATGTTGATCTGACCAAAAGCGTCTCTTACAGCTCAACAGTCTCTAGAT 951

Qy 266 HisProTrpIleGlnAsnAlaLys 273
 Db 952 CACCCGTGGTTACAGATGCAAG 975

RESULT 6

AAC47633

ID AAC47633 standard; DNA; 1836 BP.

XX AC AAC47633;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54543.

XX XX

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
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PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
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PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
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PR 18-JUN-1999; 99US-0139462P.
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PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
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PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
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PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

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Alignment Scores:

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Pred. No.: 1.09e-124 Length: 1836
Score: 1161.00 Matches: 213
Percent Similarity: 88.43% Conservative: 24
Best Local Similarity: 79.48% Mismatches: 31
Query Match: 81.82% Indels: 0
DB: 3 Gaps: 0

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US-08-989-881-2 (1-274) x AAC47633 (1-1836)

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Qy 6 GlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThr 25
Db 391 GAGATCGAGTCTAAATACACGTTGGGAGAGAGCTAGGTCGTGGAGAAATTCGGTGTACG 450
Qy 26 TyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerIysArg 45
Db 451 TATCTATGCTACTGATGAAGAGACAGCAGCGTTTGGTCTGTAATTCGATTTTGAAGAAG 510
Qy 46 LysLeuArgThrAlaValAspValArgArgGluValThrIleMetSerThr 65
Db 511 AAGCTGAGGACAGCTGTTGATTAAGACATGTTAGGAGAGAGGTTGAGATTATGAGGCAT 570
Qy 66 LeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrVal 85
Db 571 ATGCTGAGCATCCTTAATGTTTACTTTGAAGGAGAGACTTATGAGGATGAGCATGCTGTT 630

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Qy 86 HisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGly 105
Db 631 CATTTGGTTATGGAGCTTTTGAGAGTGCTGAATTTGTTGATAGATTGTTGCTAGAGG 690
Qy 106 HisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMet 125
Db 691 CATTATACTGAGAGAGCTGCTGCTGCTACTAAGACCATCATGAAAGTTGTTCCAGGTG 750
Qy 126 CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
Db 751 TGTCTAATAGCATGGGGTAAATGCACAGGACCTGAAACCTGAGAACTTCTTGTTTGGAAC 810
Qy 146 LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro 165
Db 811 AAGAGAGAGACTGCACCTCTTAAGCGGATTGATTTGGTCTCTCTGTTTCTTTAAACCA 870
Qy 166 GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys 185
Db 871 GCGGAGAGGTTTAAACGAAATCGTTGGTAGTCCGTACTACATGGCTCCGAGGTGCTAAA 930
Qy 186 ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 205
Db 931 CGGAATTTATGGTCCAGAGTTGATATTGGAGTGCAGGTGTAATTTCTTACATACGCTA 990
Qy 206 CysGlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArg 225
Db 991 TGTGGTGTCCCGCTTCTGGCGAGAACTGACACAGAGTTGCAAGCAATTTATTCCA 1050
Qy 226 GlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeu 245
Db 1051 TCTGTACTAGACTTCAGAAAGGACCCATGGCCCAAGGTTTCTGAAACGCAAAAGACCTT 1110
Qy 246 ValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnValLeuAsp 265
Db 1111 ATCAGGAAATGCTTGATCTCTGACCAAAAGCGTCTCTTACAGCTCAACAAAGTCTAGAT 1170
Qy 266 HisProTrpIleGlnAsnAlaLys 273
Db 1171 CACCGGTGTTACAGAAATGCNAG 1194

RESULT 7
AAF74280
ID AAF74280 standard; DNA; 1967 BP.
XX AAF74280;
AC AAF74280;
XX
DT 04-MAY-2001 (first entry)
XX
DE Strawberry calcium dependent protein kinase clone.
XX
KW Calcium dependent protein kinase; CDPK; herbicide resistance; paraquat;
KW diquat; crop production; ds.
XX
OS Fragaria x ananassa.
XX
PN WO200107592-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-GB002876.
XX
PR 27-JUL-1999; 99GB-00017642.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
DR WPI; 2001-168549/17.
XX
PT Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole.
XX

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Db 1140 CCATGGATTTCAGAACGCAAGAAA 1163

RESULT 10

ID ADA69918 standard; DNA; 1770 BP.

XX ADA69918;

AC ADA69918;

XX 20-NOV-2003 (first entry)

DT Rice gene, SEQ ID 3241.

DE Plant; bacterial infection; fungal infection; viral infection; rice;

XX gene; ds.

KW Oryza sativa.

XX WO2003000898-A1.

PN 03-JAN-2003.

PD 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

PR (SYGN) SYNGENTA PARTICIPATIONS AG.

PA Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

PI WPI; 2003-175290/17.

XX

DR Identifying at least one gene involved in plant resistance or response to

PT pathogenic infection for conferring resistance or tolerance to a plant to

PT bacterial, fungal or viral infection by determining or detecting plant

PT gene expression.

XX Claim 6; SEQ ID NO 3241; 899pp; English.

XX

PS The present invention relates to a method (M1) for identifying genes

XX involved in plant resistance or response to pathogenic infection. M1

CC comprises identifying a gene whose expression is significantly altered in

CC the incompatible interaction of plant gene expression relative to

CC the expression of the gene in an uninfected plant, in a mutant plant that

CC does not express a gene associated with response to pathogenic infection,

CC or in a corresponding incompatible or compatible interaction. (M1) is

CC useful for conferring resistance to resistance or tolerance to a plant to

CC bacterial, fungal or viral infection. The present sequence was used to

CC illustrate the invention.

XX

SQ Sequence 1770 BP; 449 A; 394 C; 544 G; 383 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,48e-121	Length:	1770
Score:	1132.00	Matches:	211
Percent Similarity:	88.06%	Conservative:	25
Best Local Similarity:	78.73%	Mismatches:	0
Query Match:	79.77%	Indels:	0
DB:	8	Gaps:	0

US-08-989-881-2 (1-274) x ADA69918 (1-1770)

Qy 7 IleSerAspLysTyrIleLeuGluLeuGlyArgGluPheGlyIleThrTyr 26

Db 217 ATCGACGACAAAGTACGCGGAGCTCGGGCGGGGGAGTTTCGGGGTGACGTAC 276

Qy 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46

Db 277 CTGTGATGATCGGACACCAAGAGCTCTCCCTGCAAGTCCATCTCAAGCGGAAG 336

Qy 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66

Db 337 CTGAGGACGGCGTTCGACGTTGGAGGAGTCCGCCCGGGAGTCCCATCATGCCACCTC 396

Qy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86

Db 397 CCCAAGAGCGCCAGCATCGTCTCGCGGAGGCGTGGAGGAGCAGGCGCGGTGCAC 456

Qy 87 LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaAsgGlyHis 106

Db 457 CTCGTATGAGCTCTCGAAGCGGGAGCTCTTCAGCCGATCGTGGAGGTCGTCAGCTGC 516

Qy 107 TyrThrGluArgAlaAlaThrValAlaAArgThrIleAlaGluValValArgMetCys 126

Db 517 TACACGAGCGCGCGCCCAATGTACCCGACCATCGTGGAGGTCGTCAGCTGC 576

Qy 127 HisValAsnGlyValMetHisArgAspLeuLeuPheProGluAsnPheLeuPheAlaAsnLys 146

Db 577 CACCGCCACGGCGTTATCCACCGGACCTCAAGCCCGAGAACTTCTCTTCGCGCAACAG 636

Qy 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166

Db 637 AAGGAACTCGCCGCTCAAGGCCATCGATTTCCGGCTCTCCATCTTCTTCAAGCCCGT 696

Qy 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186

Db 697 GAGAACTTTCTGAATTTGGGAAGCCCATATTACATGGCTCCAGAGGTATTGAACAGA 756

Qy 187 AsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeuTyrIleLeuLysCys 206

Db 757 AACTATGGTCCGAAATAGATATTGGAGTGCAGGAGTTATCTTGTATATTTTGTATGT 816

Qy 207 GlyValProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226

Db 817 GGAGTTCTCCATTTTGGGCTGAGACTGAGCAAGGGTGGCACAAGCCATCTTCGTGGA 876

Qy 227 ValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSerAlaLysSerLeuVal 246

Db 877 AATATCGATTTCAACGCGAACCTCGCCCAATGTTTTCAGAAAATGCTAAAGATTGGTT 936

Qy 247 LysGlnMetLeuGluProAspSerThrLysArgGluThrAlaGlnGlnValLeuAspHis 266

Db 937 CGACGATGTTGGAGCTCATCCAAACTCAGGTTAACTGCAAGCAAGTCTTGAACAT 996

Qy 267 ProTyrIleGlnAsnAlaLysLys 274

Db 997 CCATGGCTTCAAAATGCTAAGAAA 1020

RESULT 11

ADJ39574

ID ADJ39574 standard; cDNA; 1770 BP.

XX ADJ39574;

XX 06-MAY-2004 (first entry)

XX Plant cDNA #574.

XX Plant; gene; ss; transcription; plant genome augmentation; cereal;

XX soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;

XX maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;

XX stress tolerance; salt tolerance; cold tolerance; drought tolerance;

XX plant nutrition; apical dominance; dwarfism; early flowering; antiviral;

XX antifungal.

XX Eukaryota.

XX US2004016025-A1.

XX 22-JAN-2004.

XX 26-SEP-2002; 2002US-00260238.

XX 26-SEP-2001; 2001US-0325277P.

XX 26-SEP-2001; 2001US-0325448P.

XX 04-APR-2002; 2002US-0370620P.

```

XX PA (BUDW/) BUDWORTH P.
XX PA (MOUG/) MOUGHAMER T.
XX PA (BRIG/) BRIGGS S P.
XX PA (COOP/) COOPER B.
XX PA (GLAZ/) GLAZEBROOK J.
XX PA (GOFF/) GOFF S A.
XX PA (KATA/) KATAGIRI F.
XX PA (KREP/) KREPS J.
XX PA (PROV/) PROVART N.
XX PA (RICK/) RICHE D.
XX PA (ZHUT/) ZHU T.
XX
XX PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
XX PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX
XX DR WPI; 2004-190374/18.
XX
XX
XX PT New rice promoter, useful for manipulating crop plants to alter or
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX PT or high nutritional value.
XX
XX PS Claim 70; SEQ ID NO 574; 230bp; English.
XX
XX CC The invention relates to plant nucleotide sequences that direct seed-,
XX CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
XX CC or constitutive transcription of an operatively linked nucleic acid
XX CC segment. The invention also relates to a method for augmenting a plant
XX CC genome and a method of identifying a gene, where its expression is
XX CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
XX CC encode are useful for manipulating crop plants to alter or improve
XX CC phenotypic characteristics, to produce large quantities of oil or
XX CC proteins, to incur resistance to insecticides, viruses or fungi, and to
XX CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
XX CC have a high nutritional value with reduced apical dominance or dwarfism,
XX CC early flowering or altered metabolic pathways. This sequence represents a
XX CC plant nucleic acid of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification but was obtained in
XX CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 1770 BP; 449 A; 394 C; 544 G; 383 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,48e-121 Length: 1770
Score: 1132.00 Matches: 211
Percent Similarity: 88.06% Conservative: 25
Best Local Similarity: 78.73% Mismatches: 32
Query Match: 79.77% Indels: 0
DB: 12 Gaps: 0

US-08-989-881-2 (1-274) x ADJ39574 (1-1770)

Oy 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
Db 217 ATCCACGACCAAGTACCGCTCGACCGGAGCTCGCGCGGGGAGTTCCGGGTGACGTAC 276
Oy 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
Db 277 CTGTGCATGATCGGGACACCAAGAGAGCTGCTCCCTGCAAGTCACTCCACGCGAAG 336
Oy 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66
Db 337 CTGAGGACGGCGGTGCGACGTGGAGGACGTGCGCGGAGGTGCGCATCATCGCCACCTC 396
Oy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db 397 CCCAAGAGCGCCAGCATCGTCTCGTCGGGAGCGGTGCGAGGACGAGGGCGCGTGCAC 456
Oy 87 LeuValMetGluLeuLysGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106

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Db 457 CTCGTCATGGAGCTCTGGAGGCGGGAGGCTCTTCGACCGCATCGTCGCGGGGCCAC 516
Oy 107 TyrThrGluArgAlaAlaAlaThrValAlaAargThrIleAlaGluValValargMetCys 126
Db 517 TACACGGAGCGCGCGCGCAATGTCAACCCGACCATCGTGGAGGTGCTCCAGCTGCG 576
Oy 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
Db 577 CACCGCCACGCGGTATCCACCGGAGCTCAAGCCCGAGAACTTCCTCTTCGCCAACAG 636
Oy 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
Db 637 AAGGAGAACTCGCGCTCAAGGCCATCGATTTTCGCGCTCTCCATCTTCTCAAGCCCGT 696
Oy 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
Db 697 GAGAAGTTTCTGAAATTTGGGAAGCCCATATTACATGGCTCCAGAGGTATTGAAGAGA 756
Oy 187 AsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeuTyrIleLeuLysCys 206
Db 757 AACTATGTCGCGAAATAGATATTGGAGTGCAGAGTATCTTGTATATTATTATATGT 816
Oy 207 GlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
Db 817 GGAGTTCCTCCATTTTGGGCTGAGACTGAGCAAGGGGTGGCACAGCCATTTCTTCGTGA 876
Oy 227 ValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSerAlaLysSerLeuVal 246
Db 877 AATATCGATTTCAACCGCAACCTCGCCAAATGTTTCAGAAAAATGCTAAAGATTTGGTT 936
Oy 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
Db 937 CGAGCGCATGTGGAGCGCTGATCCAAAACACTCAGGTAACTGCAAAAGCAAGTTCTTGAACAT 996
Oy 267 ProTrpIleGlnAsnAlaLysLys 274
Db 997 CCATGGCTTCAAAATGCTAAGAA 1020
RESULT 12
ABZ14499
ID ABZ14499 standard; DNA; 1602 BP.
XX AC ABZ14499;
XX DT 21-JAN-2003 (first entry)
XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2304.
XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX OS Arabidopsis thaliana.
XX PN WO200216655-A2.
XX PD 28-FEB-2002.
XX PF 24-AUG-2001; 2001WO-US026685.
XX PR 24-AUG-2000; 2000US-0227866P.
XX PR 26-JAN-2001; 2001US-0264647P.
XX PR 22-JUN-2001; 2001US-0300111P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX PI Harper JF, Kreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX
XX PT Identifying a stress condition to which a plant cell has been exposed and
XX PT producing plants with increased tolerance to these abiotic stresses.

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PS Claim 144; SEQ ID NO 2304; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present invention is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office

XX SQ Sequence 1602 BP; 483 A; 265 C; 444 G; 410 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8,23e-121 Length: 1602
Score: 1127.00 Matches: 211
Percent Similarity: 88.06% Conservatve: 25
Best Local Similarity: 78.73% Mismatches: 32
Query Match: 79.42% Indels: 0
DB: 6 Gaps: 0

US-08-989-881-2 (1-274) x ABZ14499 (1-1602)

QY 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGluPheGlyIleThrTyr 26
DB 157 ATATCTTATGATGATCTGGCGGTGAGTTGGTCGCGAGAGTTGGTATTACTTAC 216
QY 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
DB 217 TTGTGCACTGATATCAAAACGGCGAGAGTATGCGTGAAGTCTATATCAAGAAGAAG 276
QY 47 LeuArgThrAlaValAspValGluAspValArgValArgValThrIleMetSerThrLeu 66
DB 277 CTTAGAACAGCTGTGGATATAGAGGATGTTAGAGGGAAGTTGAGATATGAACATATG 336
QY 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
DB 337 CCTAGACACCAATATCGTGCCTGAAGGATGCTTGGAGGATGATGATGATGATGATG 396
QY 87 LeuValMetGluLeuGlyGluGlyGluLeuPheGlyValAlaArgGlyHis 106
DB 397 ATAGTTATGAGTTGTGTAAGGAGGTGAGCTGTTGATCGGATGTTGCTAGAGTGCAT 456
QY 107 TyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys 126
DB 457 TATACTGAGCGAGCTGCTGCTGAGTATGAAGACTATTCTTCAAGTTGTTCAAGATGC 516
QY 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
DB 517 CATAAGCATGGAGTGTATGATCGGGATCTAAAGCCTGAGAAGTTCTCTTTGCAAAATAA 576
QY 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
DB 577 AAAGACATACACCCCTAAAGCCATAGATTTGGATTATCAGTCTCTTCAAGCCTGTT 636
QY 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
DB 637 GAGGGATTCAACGAGATTGTTGGAAGTCTTATTACATGCGCACGAGGTTACTTAGCGGA 696
QY 187 AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysCys 206
DB 697 AATTACGGACCTGAGTTGATATCTGGAGTGTGAGGATATCTCTTATATCTTCTGCTGT 756
QY 207 GlyValProPheThrPalaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
DB 757 GGTGTCCACCATTTGGGCGAGACTGACCAAGGGGTGCTCAGCGCATCATTAGGTCA 816
QY 227 ValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuVal 246

DB 817 GTTATCGACTTTAAGAGGGATCCATGGCGGAGAGTTTCTGAGACTGCCAAAGACCTTGTG 876
QY 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
DB 877 AGGAAGATCTCTGAACCTTGACCCCAAAACCGCTTTCTGCTGCACAAGTACTCGAACAT 936
QY 267 ProTrpIleGlnAsnAlaLysLys 274
DB 937 TCTTGATACAAATGCGAAGAG 960

RESULT 13

AAF74263

ID AAF74263 standard; DNA; 1726 BP.

XX AAF74263;

XX 04-MAY-2001 (first entry)

XX Arabidopsis calcium dependent protein kinase clone 15-1.

XX Calcium dependent protein kinase; CDPK; herbicide resistance; paraquat;

XX diquat; crop production; ds.

XX Arabidopsis sp.

XX WO200107592-A2.

XX 01-FEB-2001.

XX 26-JUL-2000; 2000WO-GB002876.

XX 27-JUL-1999; 99GB-00017642.

XX (ZENE) ZENECA LTD.

XX Holt CD, White AJ, Michael AJ, Osborn RW;

XX WPI; 2001-168549/17.

XX Producing herbicide resistance plants by inhibiting calcium dependent protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole.

XX Claim 17; Page 32; 50pp; English.

XX The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance

XX SQ Sequence 1726 BP; 518 A; 279 C; 449 G; 480 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9,14e-121 Length: 1726
Score: 1127.00 Matches: 211
Percent Similarity: 88.06% Conservatve: 25
Best Local Similarity: 78.73% Mismatches: 32
Query Match: 79.42% Indels: 0
DB: 4 Gaps: 0

US-08-989-881-2 (1-274) x AAF74263 (1-1726)

QY 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGluPheGlyIleThrTyr 26
DB 51 ATATCTTATGATGATCTGGCGGTGAGTTGGTCGCGAGAGTTGGTATTACTTAC 110
QY 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
DB 111 TTGTGCACTGATATCAAAACGGCGAGAGTATGCGTGAAGTCTATATCAAGAAGAAG 170
QY 47 LeuArgThrAlaValAspValGluAspValArgValArgValThrIleMetSerThrLeu 66

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Db 171 CTTAGAACAGCTGTGGATATAGAGGATGTTAGGAGGAAGTTGAGATAATCAACATATG 230
Qy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db 231 CCTAGACACCAATATCGTCTCGCTGAAGATGCTTTGAGGATGATGATGCGATGCGAT 290
Qy 87 LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgGlyLeuValAlaArgGlyHis 106
Db 291 ATAGTTATGGATGTTGTTGAGGAGGTTGAGTGTGTTGATCGATGTTGTTGATGATCAT 350
Qy 107 TyrThrGluArgAlaAlaThrValAlaAlaThrValAlaAlaThrValAlaAlaThrVal 126
Db 351 TATATCTGAGCGAGCTGCTGCTGCGATGATGAAGACTATCTTGAAGTTGTTGATGATGCG 410
Qy 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
Db 411 CATAAGCATGAGTGATGATCGGATCTAAAGCTGAGAACTTTCTCTTTGCAATAAA 470
Qy 147 LysGluAsnSerAlaLeuLysAlaAlaThrValAlaAlaThrValAlaAlaThrVal 166
Db 471 AAAGAGACATCAGCCCTTAAAGCCATAGATTTTGGATTTAGATTTCTTCTTCAAGCTGGT 530
Qy 167 GluArgPheThrGluLeuValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
Db 531 GAGGATTTCAACGAGATGTTTGAAGTCTTATTATACATGGCACCAGAGGTACTTATAGCGA 590
Qy 187 AsnTyrGlyProGluValAspValTrpSerAlaGlyValLysLeuLysLeuLysCys 206
Db 591 AATTACGAGCTGAGTGTATGATGATGAGTCTGAGTGTATCTTTATATCTCTCTGT 650
Qy 207 GlyValProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaLeuLysArgGly 226
Db 651 GGTGTCCACCATTTTGGCCGACACTGAGCAAGGGTGGCTCAGCGCATCATTAGGTCA 710
Qy 227 ValLeuAspPheLysArgAspProTrpSerGlnLysSerGluSerAlaLysSerLeuVal 246
Db 711 GTTATCGACTTAAAGAGGATCCATGCGGAGAGTTTCTGAGACTGCCAAGACCTTGTG 770
Qy 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 265
Db 771 AGGAAGATGCTCGAACCTGACCCCAAAAACGGCTTTCTGCTGCACAAGTACTCGAACAT 830
Qy 267 ProTrpIleGlnAsnAlaLysLys 274
Db 831 TCTTGGATACAAAATGGAGAAG 854
RESULT 14
ID ADF38032
XX ADF38032 standard; cDNA; 1868 BP.
AC ADF38032;
XX
DT 12-FEB-2004 (first entry)
XX
DE Synchronised tobacco BY2 cDNA sequence SEQ ID NO:91.
XX
KW identification; validation; plant; agrochemical; gene; ss.
XX
OS Nicotiana tabacum.
XX
PN WO2003085115-A2.
XX
PD 16-OCT-2003.
XX
FF 08-APR-2003; 2003WO-EP003703.
XX
PR 10-APR-2002; 2002EP-00447062.
PR 15-JUL-2002; 2002US-0396124P.
XX
XX (CROP-) CROPEDESIGN NV.
PA
XX Inze D, Broekaert W;
PI
XX
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DR XX WPI; 2003-804308/75.
PT Identifying and validating plant genes or proteins as targets for
PT agrochemicals, useful for producing agrochemical-resistant plants,
PT comprises determining and down regulating the gene or protein expression
PT profiles of a plant.
XX
PS Claim 12; SEQ ID NO 91; 183pp; English.
XX
CC The present invention describes a method for identifying and validating
CC plant genes/proteins as targets for agrochemicals comprising determining
CC the gene or protein expression profiles of a plant and downregulating the
CC expression of the gene or protein in the plant or plant cell. Also
CC described: (1) methods for screening candidate agrochemical compounds,
CC comprising the use of the above method or the use of any of the 785 fully
CC defined nucleotide sequences (ADP37942 to ADF38726) or protein sequences,
CC or their homologues, functional fragments or derivatives; (2) a method
CC for producing an agrochemical resistant plant, comprising the use of the
CC above-mentioned nucleotide or protein sequences; (3) an isolated nucleic
CC acid that is identified by any of the above methods or that comprises at
CC least a part of a nucleic acid sequence chosen from any of the 785
CC nucleotide sequences given in the specification; (4) a plant tolerant to
CC an agrochemical, in which the expression level of one or more of the
CC nucleic acid sequences given in the specification is modulated; and (5) a
CC harvestable part of the plant described above. The method is useful in
CC identifying and validating plant targets for agrochemicals or in
CC producing an agrochemical resistant plant. The nucleic acid or protein
CC can be used as a target for an agrochemical compound, particularly
CC herbicide. The present sequence represents a synchronised tobacco BY2
CC cDNA nucleotide sequence which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 1868 BP; 553 A; 328 C; 470 G; 517 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.: 2,28e-120 Length: 1868
Score: 1124.00 Matches: 209
Percent Similarity: 87.41% Conservative: 27
Best Local Similarity: 77.41% Mismatches: 34
Query Match: 19.21% Indels: 0
DB: 10 Gaps: 0
US-08-989-881-2 (1-274) x ADF38032 (1-1868)
Qy 5 ThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIle 24
Db 235 TCGAACGTTGAAGAGAGTATTATTAGTTGATAGAGAACTAGCGAGGGCGGAATTCGGAAT 294
Qy 25 ThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLys 44
Db 295 ACATACCTTTGTATAGATCGTAACAGTAAAGAGCTTTAGCTTCCAAGTCAATTTCAAAA 354
Qy 45 ArgLysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSer 64
Db 355 CGGAAGCTACGAACAGCTGTAGATGTGGAAGAGCTGAGGAGAGAGTAGCCATAATGAAG 414
Qy 65 ThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThr 84
Db 415 CATTTGCCGCTGAATTCGAAGTATTGTGAGCTTTAGAGAAAGCTTGTGAGGATGAAAATGCG 474
Qy 85 ValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgGlyLeuValAlaArg 104
Db 475 GTGCATTTGTTATGGAATTTGCGAAGGTGGGGAATTTGTCATAGGATTTGGCCGGA 534
Qy 105 GlyHisTyrThrGluArgAlaAlaAlaThrValAlaAlaArgThrIleAlaGluValValArg 124
Db 535 GGACATTTATCTGAACGAGCTGCTGCTGTGTACACGGACGATTTGGGAGGTTGTGATG 594
Qy 125 MetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAla 144
Db 595 CTTTGTGCTAAGCATGCTGTGATTCATCGAGATTTGAAACCTGAGAACTTTTGTATGCT 654
Qy 145 AsnLysLysGluAsnSerAlaLeuLysAlaAlaAspPheGlyLeuSerValLeuPheLys 164
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Db 655 AATAAGAGAAATTCGCCCTCTTAAAGCTATTGATTTTGGCTGTGCAATTTCTTCAAG 714
Qy 165 ProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeu 184
Db 715 CCAGGTGAGAGGTTCCTGAAATAGTCGGAAGTCCCTATTATATGCTCTCGAGGTGCTC 774
Qy 185 LysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeu 204
Db 775 AAACGAAATCATGGACCAAAATAGATATATGAGTGCAGGAGTCAATTTATATATTTTG 834
Qy 205 LeuCybGlyValProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeu 224
Db 835 TTATGTGGGGTTCCTCTTTTGGCGGAATCTGAACAAGGTGTTCCTCAGGCCATCTTA 894
Qy 225 ArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSer 244
Db 895 CGTGGGTGATAGATTCAAAACGGGAACCTGGCCCAAGTATTTTCAGAGAGTGCTAAAAAT 954
Qy 245 LeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnValLeu 264
Db 955 CTTGTACGGCAATGCTGAACACAGATCCAAAGCTTCGACTGACTGCAAAACAAGTACTT 1014
Qy 265 AspHisProTrioIleGlnAsnAlaLysLys 274
Db 1015 GAACACTCTTGGCTTCAAAATGCTAAGAG 1044

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RESULT 15

ADA70638

ID ADA70638 standard; DNA; 1515 BP.

XX AC ADA70638;

XX 20-NOV-2003 (first entry)

DE DE Rice gene, SEQ ID 3961.

XX Plant; bacterial infection; fungal infection; viral infection; rice;

XX KW gene; ds.

XX OS Oryza sativa.

XX WO200300898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to

XX pathogenic infection for conferring resistance or tolerance to a plant to

XX bacterial, fungal or viral infection by determining or detecting plant

XX gene expression.

XX Claim 6; SEQ ID NO 3961; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes

XX involved in plant resistance or response to pathogenic infection. M1

XX comprises identifying a gene whose expression is significantly altered in

XX the incompatible interaction of plant gene expression relative to

XX expression of the gene in an uninfected plant, in a mutant plant that

XX does not express a gene associated with response to pathogenic infection,

XX or in a corresponding incompatible or compatible interaction. (M1) is

XX useful for conferring resistance to resistance or tolerance to a plant to

XX bacterial, fungal or viral infection. The present sequence was used to

CC illustrate the invention.

XX SQ Sequence 1515 BP; 395 A; 344 C; 467 G; 309 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.9e-119 Length: 1515
 Score: 1115.00 Matches: 207
 Percent Similarity: 88.30% Conservative: 27
 Best Local Similarity: 78.11% Mismatches: 31
 Query Match: 78.58% Indels: 0
 DB: 8 Gaps: 0

US-08-989-881-2 (1-274) x ADA70638 (1-1515)

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Qy 10 LysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyrLeuCybThr 29
Db 187 CGGTACGAGCTCGCGCGGAGTTCGGGCGCGCGAGTTCGGGATCACGTACCTGTGCACG 246
Qy 30 AspArgGluThrArgGluAlaLeuAlaCybLysSerIleSerLysArgLysLeuArgThr 49
Db 247 GAGCGGAGACGGGACAGGTACCGTGCAGTGCATATCGAAGGGAAGCTGCGGACG 306
Qy 50 AlaValAspValGluAspValArgArgGluValThrIleMetSerThrLeuProGluHis 69
Db 307 CCGGTGGACGTGGAGACGTGCGCGGAGGTGGAGATCATGCCCAATGCGCTGCGCAT 366
Qy 70 ProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMet 89
Db 367 CCGAATCATGTCAGCTCGCGCCCTACGAGGACGAGCAACCGTGCACCTCGCATG 426
Qy 90 GluLeuCybGluGlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGlu 109
Db 427 GAGCTCTCGGAGGCGGCGAGCTCTTCGACAGATCGTCCGCGGGGCCACTACACGAG 486
Qy 110 ArgAlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCysHisValAsn 129
Db 487 CGCGCGCGCGCGCGTCAACGAGGAGTGGTTCAGATGTGCCACAGCAT 546
Qy 130 GlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsn 149
Db 547 GGTGTATGTCACCGGACCTTAAACCAAGAACTTCCTATATGCTAACCAAGAGGATAGT 606
Qy 150 SerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPhe 169
Db 607 TCTCTCTGAGGCAATTGATTTTGGGCTATCTGTGTTCTTCAGGCTCGTGAGCGGTTT 666
Qy 170 ThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGly 189
Db 667 ACTGAAATTTAGGCAGTCCATATTACATGGCTCCAGAGGTTTAAAGCGACACTATGTC 726
Qy 190 ProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuCybGlyValPro 209
Db 727 CTTGAAGTTGATGCTGGAGTGCAGAGTGATCTTACATACTCTTTTCGGGTGTACCA 786
Qy 210 ProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGlyValLeuAsp 229
Db 787 CCATTTTGGCAGAAACCGAGGAGTAGCGAGGCAATTTATACGCTCTGTGTGTAGAT 846
Qy 230 PheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuValLysGlnMet 249
Db 847 TTCAAAAGAGAACCATGGCCAGGGTATCTGAGCCAGCTAAAGATCTTCTTAAAGCGGATG 906
Qy 250 LeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHisProTyrPile 269
Db 907 TTGGACCCCAATTCCTGCAAGGCTTACTGCAGAACAAAGTACTTGAACATCATCGTTA 966
Qy 270 GlnAsnAlaLysLys 274
Db 967 CATGATTTCTAAAAG 981

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	792.5	55.8	4162	3 US-08-459-504B-26
4	792.5	55.8	4162	3 US-08-459-444-26
5	792.5	55.8	4162	3 US-09-547-422-26
6	792.5	55.8	4162	4 US-09-988-462-26
7	792.5	55.8	4165	1 US-07-951-715A-26
8	699	49.3	1349	1 US-07-951-715A-20
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22	514	36.2	1442	4	US-09-949-016-1590	Sequence 1590, Ap
23	514	36.2	1442	4	US-09-949-016-1591	Sequence 1591, Ap
24	514	36.2	1480	4	US-09-016-434-1454	Sequence 1454, Ap
25	509	35.9	2447	4	US-09-960-643-1	Sequence 1, Appl
26	508	35.8	2218	4	US-09-820-790B-1	Sequence 1, Appl
27	506	35.7	1458	4	US-09-230-896C-5	Sequence 5, Appl
28	504.5	35.6	1776	3	US-08-655-352-10	Sequence 10, Appl
29	504.5	35.6	1776	3	US-09-258-016-10	Sequence 10, Appl
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31	502.5	35.4	2454	4	US-09-992-481-3	Sequence 3, Appl
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39	498	35.1	1671	4	US-09-733-388-5	Sequence 5, Appl
40	498	35.1	1671	4	US-10-446-175-5	Sequence 5, Appl
41	498	35.1	1694	4	US-09-579-664B-3	Sequence 3, Appl
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43	498	35.1	1733	4	US-09-620-312D-526	Sequence 526, App
44	495.5	34.9	2165	4	US-09-620-312D-809	Sequence 809, App
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ALIGNMENTS

RESULT 1
US-08-459-448A-26
; Sequence 26, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Db 2596 GTCCTC 2601

RESULT 2

US-08-459-595A-26
; Sequence 26, Application US/08459595A
; Patent No. 6018104

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nallini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459.595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1416..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron

LOCATION: 2367..2451
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FEATURE:
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LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-595A-26

Alignment Scores:

Pred. No.: 9 45e-92 Length: 4162
Score: 792.50 Matches: 159
Percent Similarity: 66.67% Conservative: 29
Best Local Similarity: 56.38% Mismatches: 66
Query Match: 55.85% Indels: 29
DB: 3 Gaps: 1

US-08-989-881-2 (1-274) x US-08-459-595A-26 (1-4162)

Qy 11 TyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyrLeuCysThrAep 30
Db 1757 TACTCGATGGCAAGGAGCTCGGCGCGGCGGAGTTCGGCGTGCACGACCTGTGCAGCAC 1816
Qy 31 ArgGluThrArgGluAlaLeuAlaCysGlySerIleSerIleArgLysLeuArgThrAla 50
Db 1817 CGGACGAGCGCGGAGAGCTGGCGTGCAAGCATCGCAAGCGAAGCTGGCGGCCAGG 1876
Qy 51 ValAspValGluAspValArgGluValThrIleMetSerThrLeuProGluHisPro 70
Db 1877 GAGGACGTGGACGACGTGGCGGGAGTGCAGATCATGCACACCTCTTCGGCGCAGGCC 1936
Qy 71 AsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGlu 90
Db 1937 AACGTGTGGGCTTCGCGCGCGGCTACGAGGACAAGCAGCGTGCACCTCGTCATGGAG 1996
Qy 91 LeuCysGluGlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArg 110
Db 1997 CTGTGCGGCGGGGAGCTCTTCGACCGCATCATCGCCCGGGGCCAGTACACGAGCGC 2056

QY 111 AlaAlaAlaThrValAlaAaGrThrIleAlaGluValValArgMetCysHisValAsnGly 130
Db 2057 GGGCCCGCGAGCTGTCGCGCATCGTCAGATCGTCACACCTCCACCTCCATGGG 2116
QY 131 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSer 150
Db 2117 GTGATGCCCGGACATCAAGCCGAGAACTTCTGCTGCTCAGCAAGGAGGAGCGG 2176
QY 151 AlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGluA-rgPheThr 170
Db 2177 CCGTCAAGGCCACCGACTTCGGCTCTCGCTCTCTTCAAGGAGGCGGCTGCAGG 2236
QY 171 GluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyPro 190
Db 2237 GACATCGTCGCGAGCGCTACTACATCGCCCGAGGTGCTCAAGAGAAAGTACGCGCCG 2296
QY 191 GluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysGlyValProPro 210
Db 2297 GAGCGGCACATCTGGAGCGTCGCGTCTACATCTTCTCGCGCGGTGCTCC 2356
QY 211 PheTrpAla----- 213
Db 2357 TTCTGGGC-AGTTCGGATCGCTCGTGTCTGCTCCTAGACGATATACAGAACCCGACGATG 2415
QY 214 -----GluThrGluGlnGlyValAlaLeuAla 222
Db 2416 GATTGCTTCTAGCCCTGTTTGTGATCACCAGAGAACGAGCATCTTCCACCGCC 2475
QY 223 IleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAla 242
Db 2476 ATCTGCGAGGCGAGCTTGACCTCTCCAGCGAGCATGCGCACACATCTCGCGGGAGCC 2535
QY 243 LysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGln 262
Db 2536 AAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGTCTCAGGGGTTCAG 2595
QY 263 ValLeu 264
Db 2596 GTCTC 2601

RESULT 3

US-08-459-504B-26
Sequence 26, Application US/08459504B
Patent No. 6075185

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427 /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
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NAME/KEY: exon
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NAME/KEY: intron
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LOCATION: 3714..3811

US-08-459-504B-26

Alignment Scores:
Pred. No.: 9,45e-92 Length: 4162
Score: 792.50 Matches: 159
Percent Similarity: 66.67% Conservative: 29
Best Local Similarity: 56.38% Mismatches: 66
Query Match: 55.85% Indels: 29
DB: 3 Gaps: 1

US-08-989-881-2 (1-274) x US-08-459-504B-26 (1-4162)

Qy 11 TyrIleuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyLeuCyThrAsp 30
Db 1757 TACTCGATGGCGCAAGAGCTCGGCGCGGAGTTGCGGACGACCTGTGCAGGCAC 1816
Qy 31 ArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLysLeuArgThrAla 50
Db 1817 CGGACGAGCGCGAGAGCTGGCTGCAAGCAGTCCGGAAGCGAAGCTGGCGCCAGG 1876
Qy 51 ValAspValGluAspValArgGluValThrIleMetSerThrLeuProGluHisPro 70
Db 1877 GAGCAGCTGGACGACCTCGCGCGGAGGTGCAGATCATGCACCACTCTCCGCGCCAGCC 1936
Qy 71 AsnValValLysLeuLysAlaThrTyGluAspAsnGluThrValHisLeuValMetGlu 90
Db 1937 AACGTGTGGCCCTCCGCGCGCGCTACGAGACAGCAGCGTGCACCTCGTCATGGAG 1996
Qy 91 LeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHisTyThrGluArg 110
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Qy 111 AlaAlaAlaThrValAlaAlaArgThrIleAlaGluValValArgMetCysHisValAsnGly 130
Db 2057 GCGCGCGCGAGCTCTCGCGGCCATCTGCAGATCGTGCAGATCGTGCACACCTGCCACTCCATGGG 2116
Qy 131 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSer 150
Db 2117 GTGATGACCGGGACATCAAGCCCGAGAACTTCTCTGCTGCTCAGCAGGAGGAGCGCG 2176
Qy 151 AlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPheThr 170
Db 2177 CCGCTCAAGGCCACCGACTTCGGCTCTCCGCTCTTTCAGGAGGCGGAGCTGCTCAGG 2236
Qy 171 GluIleValGlySerProTyThrMetAlaProGluValLeuLysArgAsnTyrcGlyPro 190
Db 2237 GACATCGTCGCGAGCGCCTACTACATCGCGCCGAGGTGCTCAAGAGGAAGTACGCGCCG 2296
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Qy 211 PheTrpAla----- 213
Db 2357 TTCTGGGC-AGGTCCGATCCGTCGCTGCTCTAGACATATACAGAACCCGAGCATG 2415
Qy 214 -----GluThrGluGlnGlyValAlaLeuAla 222
Db 2416 GATTGCTTCTCAGCCCTGTTCTTTCATCACAGAGAAGCAGACGCGATCTTCAACGCC 2475
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RESULT 4

US-08-459-444-26
; Sequence 26, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Lounis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1418..1427
; OTHER INFORMATION: /note= "start of mRNA"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1481..2366
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2367..2451
; FEATURE:
; NAME/KEY: exon
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; FEATURE:

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/ NAME/KEY: intron
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US-08-459-444-26

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Alignment Scores:
Pred. No.: 9.45e-92 Length: 4162
Score: 792.50 Matches: 159
Percent Similarity: 66.67% Conservative: 29
Best Local Similarity: 56.38% Mismatches: 66
Query Match: 55.85% Indels: 29
DB: 3 Gaps: 1

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US-08-989-881-2 (1-274) x US-08-459-444-26 (1-4162)

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Qy 11 TyrIleuGlyArgGluLeuGlyArgGlyPheGlyIleThrTyrLeuCysThrAsp 30
Db 1757 TACTCGATGGCAGGAGCTGGCGCGGGCAGTTCGGCGTGACGACCTGTGCACGCAC 1816
Qy 31 ArgGluThrArgGluAlaLeuAlaCysLeuSerIleSerIleArgGlyLeuAlaGThrAla 50
Db 1817 CGACAGCGCGGAGAGCTGGGTGCAGACGATCGCGAGGCGGAGCTGGCGGCGCAGG 1876
Qy 51 ValAspValGluAspValArgArgGluValThrIleMetSerThrLeuProGluHisPro 70
Db 1877 GAGGACGTGACGACGCGCGGGAGGTGCAGATCATGCACCACTCTCCGGCCAGCCC 1936
Qy 71 AsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGlu 90
Db 1937 AACGTGGTGGCCCTCCGCGCGCGGTACGAGGACAGCAGCGTGCACCTCGTCATGGAG 1996
Qy 91 LeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArg 110
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Qy 111 AlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCysHisValAsnGly 130
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Qy 131 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSer 150
Db 2117 GTGATGACCGGAGACATCAAGCCCGAGACTTCTGCTGCTCAGGAGGACGAGGAGCGG 2176
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RESULT 5

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US-09-547-422-26

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; Sequence 26, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Lounis, Karen L.
;
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE

```

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NUMBER OF SEQUENCES: 94

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```

CORRESPONDENCE ADDRESS:

```

```

ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.

```

```

STREET: 3054 Cornwallis Road

```

```

CITY: Research Triangle Park

```

```

STATE: NC

```

```

COUNTRY: USA

```

```

ZIP: 27709

```

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COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patent In Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:

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```

APPLICATION NUMBER: US/09/547,422

```

```

FILING DATE: 11-Apr-2000

```

```

CLASSIFICATION: <Unknown>

```

```

PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER: US 08/459,595

```

```

FILING DATE: 02-JUN-1995

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```

APPLICATION NUMBER: US 07/951,715

```

```

FILING DATE: 25-SEP-1992

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```

APPLICATION NUMBER: US 07/772,027

```

```

FILING DATE: 04-OCT-1991

```

```

ATTORNEY/AGENT INFORMATION:

```

```

NAME: Meigs, J. Timothy

```

```

REGISTRATION NUMBER: 38,241

```

```

REFERENCE/DOCKET NUMBER: S-18805H

```

```

TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: (919)541-8587

```

```

TELEFAX: (919)541-8689

```

```

INFORMATION FOR SEQ ID NO: 26:

```

```

SEQUENCE CHARACTERISTICS:

```

LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-547-422-26

Alignment Scores:
Pred. No.: 9,45e-92 Length: 4162
Score: 792.50 Matches: 159
Percent Similarity: 66.67% Conservative: 29
Best Local Similarity: 56.38% Mismatches: 66
Query Match: 55.85% Indels: 29
DB: 3 Gaps: 1

US-08-989-881-2 (1-274) x US-09-547-422-26 (1-4162)

Qy 11 TyrileuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyrLeuCysThrAsp 30
Db 1757 TACTCGATGGCAAGAGCTCGGGCGGGAGTTTCGGCGTGCAGAGCGGAAGCTGGCGCCAGG 1876
Qy 31 ArgGluThrArgGluAlaLeuAlaCysLysSerLysIleThrTyrLeuArgThrAla 50
Db 1817 CGGACGCGCGGAGAGCTGGGTGCAGAGCTGCAGAGCGGAAGCTGGCGCCAGG 1876
Qy 51 ValAspValGluAspValArgGluValThrIleMetSerThrLeuProGluHisPro 70
Db 1877 GAGGACGTGGACGCTGGCGGGGAGGTGCAGATCATGCACCACTCTCCGGCCAGGCC 1936

Qy 71 AsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGlu 90
Db 1937 AACGTGGTGGGCTCCGCGCGCGGTACGAGGACGAGCGGTCCCTCGTCTAGGAG 1996
Qy 91 LeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArg 110
Db 1997 CTGTGCGCGGGGGAGCTCTTCACCGCATCATCGCCCGGGGCGAGTACACGAGCGC 2056
Qy 111 AlaAlaThrValAlaArgThrIleAlaGluValValArgMetCysHisValAsnGly 130
Db 2057 GCGCGCGGAGCTGTGCGCGCATCTGTGAGATCGTCACACCTGCACCTCCATCCATGGG 2116
Qy 131 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSer 150
Db 2117 GTGATGCACCGGACATCAAGCCGAGAACTTCCTGTGCTCAGCAAGACGAGACGGG 2176
Qy 151 AlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGlyLysArgPheThr 170
Db 2177 CCGCTCAAGGCCACCGACTTCGGGCTCTCCGCTCTTCTCAAGGAGGCGAGCTGCTCAGG 2236
Qy 171 GluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyPro 190
Db 2237 GACATCGTGGCAGCGCTACTACATCGCGCCGAGGTGCTCAAGAGGAAGTACGCGCGG 2296
Qy 191 GluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuLysGlyValProPro 210
Db 2297 GAGCCGACATCTGGAGCGTGCAGCGTCTATGCTCTACATCTTCCTCGCGGGGTGCTCCG 2356
Qy 211 PheTrpAla 213
Db 2357 TTCTGGGC-AGGTGCGATCCGTCGCTGTTCTCTAGACGATATACAGAACCCGACGATG 2415
Qy 214 -----GluThrGluGlnGlyValAlaLeuAla 222
Db 2416 GATTGTCTCTCAGCCCTGTTCTTTCATCACAGAGAACGAGACGGCATCTTCACCGCC 2475
Qy 223 IleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAla 242
Db 2476 ATCTTGGAGGGCAGCTTGACCTCTCCAGCGGAGCATGGCCACACATCTCCGCGGAGGCC 2535
Qy 243 LysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGln 262
Db 2536 AAGGATCTCTCAGAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGGCGTCCAG 2595
Qy 263 ValLeu 264
Db 2596 GTCCTC 2601

RESULT 6

US-09-988-462-26
; Sequence 26, Application US/09988462
; Patent No. 6720488

GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.

Desai, Nalini M.
Lewis, Kelly S.

Kramer, Vance C.
Warren, Gregory W.

Evola, Stephen V.
Crossland, Lyle D.

Wright, Martha S.
Merlin, Ellis J.

Lauis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA


```

Db      2175  CGCTCAAGGCCACCGACTTCGGCCCTTCGGTCTTCTTCAAGGAGCGGAGCTGCTCAGG 2234
Qy      171  GluileValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyPro 190
Db      2235  GACATCGTCGGCAGCGCTACTACATCGCGCCGAGGTGCTCAAGAGGAAGTACGGCCCG 2294
Qy      191  GluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuCysGlyValProPro 210
Db      2295  GAGCGCGACATCGGAGCGTCGGCGTTCATCTCTACATCTTCTCGCGCGGCTGCTCC 2354
Qy      211  PheTrpAla----- 213
Db      2355  TTCTGGGC-AGTGGCATCGTCCGTCGTCCTAGACGATATACAGAACCGCAGCATG 2413
Qy      214  -----GluThrGluGlnGlyValAlaLeuAla 222
Db      2414  GATTTCCTCTCAGCCCTGTTCTTGCATCACCAGAGAACGAGACGCTCTTCCACCGCC 2473
Qy      223  IleLeuArgGlyValLeuAspPheLysArgAspProTyrTrpSerGlnIleSerGluSerAla 242
Db      2474  ATCCCTCGAGGCGAGCTTCACTCTCCAGCGAGCCATGGCCACACATCTCGCGGGAGCC 2533
Qy      243  LysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGln 262
Db      2534  AAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGAGCGGCTCAGCGGTTCCAG 2593
Qy      263  ValLeu 264
Db      2594  GTCCCTC 2599

```

RESULT 8

US-07-951-715A-20
Sequence 20, Application US/07951715A

Patent No. 5625136

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/951,715A

FILING DATE: 25-SEP-1992

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226 /note= "cdna sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-07-951-715A-20

Alignment Scores:

Pred. No.: 2,158-80 Length: 1349
Score: 599.00 Matches: 132
Percent Similarity: 73.68% Conservative: 22
Best Local Similarity: 63.16% Mismatches: 55
Query Match: 49.26% Indels: 0
DB: 1 Gaps: 0

US-08-989-881-2 (1-274) x US-07-951-715A-20 (1-1349)

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Qy      62  IleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAsp 81
Db      6  ATCATGACCACTCTCCGGCCAGCCCAACGCTGGTGGGCTCCGGCGCGTACGAGGAC 65
Qy      82  AsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIle 101
Db      66  AAGCAGAGCGTGCACCTGCTCATGGAGCTGTGCGCGGGCGGGAGCTCTTTCAGCCGCATC 125
Qy      102  ValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGlu 121
Db      126  ATCGCCCGGGGCCAGTACACGGAGCGCGCGCGCGGAGCTGCTCGCGCCCATGTGCAG 185
Qy      122  ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLeuProGluAsnPhe 141
Db      186  ATCGTGCACACCTGCCACTCCATGGGGGTGATGCACCGGACATCAAGCCCGAGAACTTC 245
Qy      142  LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db      246  CTGCTGCTCAGCAAGGACGAGGACGCGCGCTCAAGGCCACCGACTTCGGCTCTCCGTC 305
Qy      162  LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
Db      306  TTCITCAAGGAGGGCGAGCTGCTCAGGACATCGTCCGACGGCCCTACTACATCGCGCCC 365
Qy      182  GluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeu 201
Db      366  GAGGTGCTCAAGAGAGAGTACGGCCGCGGAGCGGCACATCTGGAGCGTCCGCGCTCATG 425
Qy      202  TyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAlaLeu 221
Db      426  TACATCTTCTCCGCGCGGTGCTCCCTTCTGGGAGAGAACGAGAACGGCATCTTCACC 485
Qy      222  AlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrTrpSerGlnIleSerGlu 241
Db      486  GCCATCTTCGAGGAGGCGAGCTTGACCTCTCCAGCGGACCATGCGCCACACATCTCGC 545
Qy      242  AlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
Db      546  GCCAAGGATCTCGTCAAGAGAGATGCTCAACATCAACCCCAAGGAGCGGCTTCACGGC 605

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Qy 262 GlnValLeuAspHisProTyrPheGln 270
Db 606 CAGGTCTCAATCAACCATGGATCAAA 632

RESULT 9

US-08-459-448A-20
; Sequence 20, Application US/08459448A
; Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA

ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,448A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8582

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note= "cDNA sequence for maize

OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as

OTHER INFORMATION: disclosed in Figure 30."

US-08-459-448A-20

Alignment Scores:

Pred. No.: 2.15e-80 Length: 1349
Score: 699.00 Matches: 132
Percent Similarity: 73.68% Conservative: 22
Best Local Similarity: 63.16% Mismatches: 55
Query Match: 49.26% Indels: 0
DB: 2 Gaps: 0

US-08-989-881-2 (1-274) x US-08-459-448A-20 (1-1349)

Qy 62 IleMetSerThrLeuProGluHisProAsnValVallyLeuLysLeuLysAlaThrTyrGluAsp 81
Db 6 ATCATGACACCTCTCCGCCAGCCCAACCTGTGTGGCCCTCCGCCGGCGGTACGAGGAC 65
Qy 82 AsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLysPheGlyArgile 101
Db 66 AAGCAGAGCGTGCACCTCGTCATGGAGCTGTCCCGGGGGGGAGCTCTTCGACCGCATC 125
Qy 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGlu 121
Db 126 ATCCCGGGGGCCAGTACACGGAGCGCGCGCGGAGCTGTCTCGACCGCATC 145
Qy 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
Db 186 ATCGTGACACCTCCACTCCATCGGGGTGTATGACCGGGGACATCAAGCCGAGAACTTC 245
Qy 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db 246 CTGCTGCTCAGCAAGGAGGAGCGCGCGCTCAAGGCCACCGACTTCGGCTCTCCGTC 305
Qy 162 LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
Db 306 TTCTTCAAGGAGGCGAGCTGCTCAGGGACATCTCGCGAGCGCTACTACTACATCGCGCC 365
Qy 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeu 201
Db 366 GAGGTGCTCAAGAGGAAGTACGGCCCGAGGCGGACATCTGGAGCGTCCGGCTCATGCTC 425
Qy 202 TyrIleLeuLysCysGlyValProPheTrpAlaGluThrGluGlnGlyValAlaLeu 221
Db 426 TACATCTTCTCGCGCGGTGCTCTCTTCTGGGACAGAACGAGACGGCATCTTACC 485
Qy 222 AlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSer 241
Db 486 GCCATCTCGAGGCGAGCTTACCTCTCCAGCGAGCATGCGCCACACATCTCGCGCGGA 545
Qy 242 AlalysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
Db 546 GCCAAGGATCTCGTCAAGAAAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGGCGTTC 605
Qy 262 GlnValLeuAspHisProTyrPheGln 270
Db 606 CAGGTCTCAATCAACCATGGATCAAA 632

RESULT 10

US-08-459-595A-20

; Sequence 20, Application US/08459595A

; Patent No. 6018104

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lytle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.

APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 607518artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-08-459-595A-20
Alignment Scores:
Pred. No.: 2,15e-80 Length: 1349
Score: 699.00 Matches: 132
Percent Similarity: 73.68% Conservative: 22
Best Local Similarity: 63.16% Mismatches: 55
Query Match: 49.26% Indels: 0
DB: 3 Gaps: 0
US-08-989-881-2 (1-274) x US-08-459-595A-20 (1-1349)
QY 62 IleMetSerThrLeuProGluHisProAsnValValLeuLysAlaThrTyrGluAsp 81
Db 6 ATCATCACACCTCTCCGGCCAGCCCAACGTGTGGGCTCCGGCGCGGTACGAGGAC 65
QY 82 AsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIle 101
Db 66 AAGCAGAGGTGCACCTCGTCATGAGAGCTGTGGCGGGCGGGAGCTCTTCGACCGCATC 125
QY 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaAlaArgThrIleAlaGlu 121
Db 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaAlaArgThrIleAlaGlu 121

Db 126 ATGCGCGGGCCAGTACACGGAGCGCGCGCGGAGTGCTGCGCGCCATCGTGCGAG 185
QY 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
Db 186 ATGCTGCACACCTGCCATCCATGGGGGTGATGACACCGGCACATCAAGCCGGAACCTTC 245
QY 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db 246 CTGCTGCTCAGCAAGGACGAGGACGGCGCTCAAGGCCACCGACTTCGGCCTCTCCGTC 305
QY 162 LeuPheLysProGlyGluArgPheThrGluIleValIglySerProTyrTyrMetAlaPro 181
Db 306 TTCTTCAAGGAGCGCGAGCTGCTCAGGGACATCGTCGGCAGCGCCTACTACATCGCGCCC 365
QY 182 GluValLeuLysArgAsnTyrGlyProGluValAlaAspValTrpSerAlaGlyValIleLeu 201
Db 366 GAGGTGCTCAAGAGGAAGTACGGCGCGGAGCGGCACATCTGGAGCGTCGCGCTCATGCTC 425
QY 202 TyrIleLeuLeuCysGlyValProPheTyrAlaGluThrGluGlnGlyValAlaLeu 221
Db 426 TACATCTTCTCGCGCGGTGCTCCCTTCTGGGCGAGAGAACGAGAACGGCATCTTCACC 485
QY 222 AlaIleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSer 241
Db 486 GCATCTCGGAGGCGAGCTTGACCTCTCCAGCGGCCATGGCCACACATCTTCGCGGGA 545
QY 242 AlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
Db 546 GCCAAGGATCTCGTCAAGAGATGTCTCAACATCAACCCCAAGGAGCGGCTCACGGGCTTC 605
QY 262 GlnValLeuAspHisProTrpIleGln 270
Db 606 CAGGTCTCTCAATCACCCTGGATCAAA 632
RESULT 11
US-08-459-504B-20
Sequence 20, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Kozel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 607518artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: /note= "cDNA sequence for maize
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-08-459-504B-20
Alignment Scores:
Pred. No.: 2,158-80 Length: 1349
Score: 699.00 Matches: 132
Percent Similarity: 73.68% Conservative: 22
Best Local Similarity: 63.16% Mismatches: 55
Query Match: 49.26% Indels: 0
DB: 3 Gaps: 0
US-08-989-881-2 (1-274) x US-08-459-504B-20 (1-1349)
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Db 6 ATCATGCACCTCTCCGGCCAGCCCAACGTGTGGGCTCCGGGGCGGTACAGGAC 65
Qy 82 AsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgile 101
Db 66 AAGCAGACGCTGCCTCTCATGAGCTGTGCGGGGGGAGCTCTTCGACCGCATC 125
Qy 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGlu 121
Db 126 ATCGCCGGGGCCAGTACACGAGCGCGCGCGGAGCTGCTCGCGCCATCTGTGCAG 185
Qy 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
Db 186 ATGTGACACCTGCCTCATATGGGGTGTATGACCGGACATCAAGCCAGCACTTCGCTC 245
Qy 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db 246 CTGCTGCTCAGCAGGAGGAGGACGCGCGCTCAAGGCCACCGACTTCGGCTCTCCGTC 305
Qy 162 LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
Db 306 TTCTTCAAGGAGGGGAGCTGTCTCAGGGACATCTGCGCAGCGGCTACTACATCCGCGCC 365
Qy 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeu 201
Db 366 GAGTGTCTCAGAGAGAGTACGCGCCGAGGCGGACATCTGGAGCGCTCGGCTCATGCTC 425
Qy 202 TyrIleLeuLysGlyValProProPheThrAlaGluThrGluGlnGlyValAlaLeu 221
Db 426 TACATCTTCTCGCGGGGTGCTCTCCCTTCTGGGAGAGAACGAGACGCGCATCTTACC 485

Qy 222 AlaIleLeuArgGlyValValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSer 241
Db 486 OCCATCTCGCGAGGCGAGCTTGACCTCTCCAGCGGAGCCATGCCACACATCTCGCGCGGA 545
Qy 242 AlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
Db 546 GCCAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGAGCGGCTCAGCGGTTTC 605
Qy 262 GlnValLeuAspHisProTyrIleGln 270
Db 606 CAGGTCTCTCAATCACCCTGATGATCAAA 632
RESULT 12
US-08-459-444-20
Sequence 0, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crosland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauais, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: /note= "cDNA sequence for maize
pollen-specific calcium dependent protein kinase gene a
disclosed in Figure 30."
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-08-459-444-20

Alignment Scores: 2.15e-80 Length: 1349
Pred. No.: 699.00 Matches: 132
Score: 73.68% Conservativeness: 22
Percent Similarity: 63.16% Mismatches: 55
Best Local Similarity: 49.26% Indels: 0
Query Match: 3 Gaps: 0
DB:

US-08-989-881-2 (1-274) x US-08-459-444-20 (1-1349)

QY 62 IleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAsp 81
DB 6 ATCATGCACACCTCTCCGCGCCAGCCCAACGTGGGCTCCGCGCGCGTACGAGGAC 65
QY 82 AsnGluThrValHisLeuValMetGluLeuLeuGluGlyGlyGluLeuPheGlyArgile 101
DB 66 AAGCAGAGCGTGACCTCGTCATGGAGCTGTGCGCGCGCGGAGCTCTTCGACCGCATC 125
QY 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaAlaArgThrileAlaGlu 121
DB 126 ATCGCCCGGCGCCAGTACACGAGCGCGCGCGCGAGCTGTGCGCGCGCATCTGTCGAC 185
QY 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
DB 186 ATCGTGCACACCTGCCACTCTCATGGGGTGATGACCGGACATCAAGCCCGAGAACTTC 245
QY 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaAlaLeuAspPheGlyLeuSerVal 161
DB 246 CTGCTCTCAGCAGGAGGAGCGCGCTCAAGGCCACCCACTTCGGCTCTCTCGTC 305
QY 162 LeuPheLysProGlyGluArgPheThrGluLeuValGlySerProTyrTyrMetAlaPro 181
DB 306 TTCTTCAAGGAGGCGAGCTGTCTCAGGACATCTCGGACGCGCTACTACATCGCGCCC 365
QY 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValileLeu 201
DB 366 GAGTGCTCAAGAGGAGTACGCGCGCGCGGCGGACATCTGGAGCGTGGCGGTCTGCTC 425
QY 202 TyrileLeuLeuLysGlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeu 221
DB 426 TACATCTCTCGCGCGCGTCTCTCTCTCTGCGGAGAGACGAGACGCGCATCTTCACC 485
QY 222 AlaileLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnileSerGluSer 241
DB 486 GCCATCTCGCGGCGAGCTTGACCTCTCCAGCGGACCATGCGGCACACATCTCGCGGGA 545
QY 242 AlaLysSerValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
DB 546 GCCAAGATCTCTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGCTTCAGCGGTTTC 605
QY 262 GlnValLeuAspHisProTrpIleGln 270
DB 606 CAGGTCTCAATCAACCCATGGATCAAA 632

RESULT 13

US-09-547-422-20
Sequence 0, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Kramer, Kelly S.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Lauis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/547,422

FILING DATE: 11-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/459,595

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805H

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: /note= "cDNA sequence for maize

pollen-specific calcium dependent protein kinase gene as

disclosed in Figure 30."

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-547-422-20

Alignment Scores:

Pred. No.: 2.15e-80 Length: 1349

Score: 699.00 Matches: 132

Percent Similarity: 73.68% Conservativeness: 22

Best Local Similarity: 63.16% Mismatches: 55

Query Match: 49.26% Indels: 0

DB: 3 Gaps: 0

US-08-989-881-2 (1-274) x US-09-547-422-20 (1-1349)

QY 62 IleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAsp 81
DB 6 ATCATGCACACCTCTCCGCGCCAGCCCAACGTGGGCTCCGCGCGCGTACGAGGAC 65
QY 82 AsnGluThrValHisLeuValMetGluLeuLysGlyGlyGluLeuPheGlyArgile 101
DB 66 AAGCAGAGCGTGACCTCGTCATGGAGCTGTGCGCGCGCGGAGCTCTTCACCGCATC 125
QY 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaAlaArgThrileAlaGlu 121
DB 126 ATCGCCCGGCGCCAGTACACGAGCGCGCGCGGAGCTGTGCGCGCGCATCTGTCGAC 185
QY 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
DB 186 ATCGTGCACACCTGCCACTCTCATGGGGTGATGACCGGACATCAAGCCCGAGAACTTC 245

Qy 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db 246 CTGCTGCTCAGCAAGGACGAGCGCGCTCAAGCCACCGACTTCGGCTCTCCGTC 305
Qy 162 LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
Db 306 TTCTTCAAGGAGGCGAGCTCTCAGGACATCGTCGCGAGCGCTACTACATCGCGCC 365
Qy 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeu 201
Db 366 GAGGTGCTCAGAGAGAGTACGCGCGGAGCGGACATCTCGAGCGTCTGGCGTCTATGTC 425
Qy 202 TyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAlaLeu 221
Db 426 TACATCTCTCCGCGCGTCCCTCTCTGGGAGAGAACGAGCGGATCTTACC 485
Qy 222 AlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSer 241
Db 486 GCCATCTCGAGGCGAGCTTGACCTCTCCAGCGGACATCGCCACACATCTCGCGGGA 545
Qy 242 AlalysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
Db 546 GCCAAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGCGTTC 605
Qy 262 GlnValLeuAspHisProTyrIleGln 270
Db 606 CAGGTCTCTCAATCAATCAATGATCAAA 632

RESULT 14

US-09-988-462-20
; Sequence 20, Application US/09988462

; Patent No. 6720488

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-No. 6720488-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1326
; OTHER INFORMATION: /note="cDNA sequence for maize
; pollen-specific calcium dependent protein kinase gene as
; disclosed in Figure 30."
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-988-462-20

Alignment Scores:
Pred. No.: 2,15e-80 Length: 1349
Score: 699.00 Matches: 132
Percent Similarity: 73.68% Conservative: 22
Best Local Similarity: 63.16% Mismatches: 55
Query Match: 49.26% Indels: 0
DB: 4 Gaps: 0

US-08-989-881-2 (1-274) x US-09-988-462-20 (1-1349)

Qy 62 IleMetSerThrLeuProGluHisProAsnValLysLeuLysAlaThrTyrGluAsp 81
Db 6 ATCATGCACCACCTCTCCGCGCAGCCCAACGCTGGTGGCGCTCCCGCGCGCTAGAGGAC 65
Qy 82 AsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIle 101
Db 66 AAGCAGAGCGTGACCTCTGTCATGGAGCTGTGCGCGCGCGGGAGCTCTTCGACCGCATC 125
Qy 102 ValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaLeaThrIleAlaGlu 121
Db 126 ATGCCCGCGGCGCAGTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 185
Qy 122 ValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPhe 141
Db 186 ATCGTGACACCTGCCACTCCATGGGGGTGATGCACCGGAGCATCAAGCCGAGAACTTC 245
Qy 142 LeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerVal 161
Db 246 CTGCTGCTCAGCAAGGACGAGCGCGCGCTCAGGCGCGCGCGCGCGCGCGCTCTCCGTC 305
Qy 162 LeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaPro 181
Db 306 TTCTTCAAGGAGGCGAGCTCTCAGGACATCGTCGCGAGCGCTACTACATCGCGGCC 365
Qy 182 GluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeu 201
Db 366 GAGGTGCTCAAGAGGAAAGTACGCGCGGAGCGGACATCTGGAGCGTCTGGCGTCTATGTC 425
Qy 202 TyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAlaLeu 221
Db 426 TACATCTCTCCGCGCGTCCCTCTCTGGGAGAGAACGAGCGGATCTTACC 485
Qy 222 AlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSer 241
Db 486 GCCATCTCGAGGCGAGCTTGACCTCTCCAGCGGAGCATCGCCACACATCTCGCGGGA 545
Qy 242 AlalysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGln 261
Db 546 GCCAAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGCGTTC 605
Qy 262 GlnValLeuAspHisProTyrIleGln 270

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Db      606 CAGGTCTCAATCACCCATGATCAAA 632
RESULT 15
US-09-347-801-3
; Sequence 3, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 2374
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-347-801-3

Alignment Scores:
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Percent Similarity: 65.06%      Conservative: 38
Best Local Similarity: 50.93%      Mismatches: 90
Query Match:      49.12%      Indels:      4
DB:               3          Gaps:      2

US-08-989-881-2 (1-274) x US-09-347-801-3 (1-2374)
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Qy      30 AspArgGluThrArg-----GluAlaLeuAlaCysLysSerIleSerLysArgLys 46
Db      765 GTCGAAGAGGGCGAGTACAGGACAGACCGTCGCGCTCAAGATCATCGCCAAAGCTAAG 824
Qy      47 LeuArgThrAlaValAspValArgGluLeuPheGlyValThrIleMetSerThrLeu 66
Db      825 ATGACAACGCGCATATCCATTGAGGATGTCGTAGAGAGTAAATTTTGAGAGCGTTA 884
Qy      67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db      885 TCAGGGCACAAATAATCTCGTCAAAATTCATGATGCATGTGAGGATGCGCTCAATGTCTAC 944
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Db      945 ATTGTGATGAATATGTGAGGAGGAGAAATTCGTAGACAGAAATATTAGCCAGAGGGGG 1004
Qy      106 HisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMet 125
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Qy      126 CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
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Db      1185 GATGAAGGCTTAATGATATTTGGAAGTGCATATTATGTTGCCCCACAGAGGTTTACAC 1244
Qy      186 ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 205
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Job time : 194 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: October 14, 2005, 17:02:14 : Search time 756 Seconds
(without alignments)
2540.626 Million cell updates/sec

Title: US-08-989-881-2

Perfect score: 1419

Sequence: 1 MANQIQISKYILGRELGRG.....TKRLTAQQVLDHPWQNAKK 274

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Searched: 8755912 seqs, 3504951483 residues

Total number of hits satisfying chosen parameters: 17531824

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Post-processing: Minimum Match 0%

Maximum Match 100%

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-THR_MIN=0 -ALIGN=15 -NODE=LOCAL -OUTFMT=pcr -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US08989881 @cgn_1_1_886 @runat_14102005_112731_5122
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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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4	1252	88.2	2628	18	US-10-424-599-37843	Sequence 37843, A
5	1246	87.8	1787	18	US-10-425-114-10952	Sequence 10952, A
6	1164	82.0	2126	18	US-10-424-599-57457	Sequence 57457, A
7	1155	81.4	1978	19	US-10-437-963-7404	Sequence 7404, Ap
8	1147	80.8	2149	18	US-10-425-114-34236	Sequence 34236, A
9	1143	80.5	2244	18	US-10-425-114-28411	Sequence 28411, A
10	1143	80.5	2298	20	US-10-425-115-28928	Sequence 28928, A
11	1136	80.1	2274	18	US-10-425-114-24006	Sequence 24006, A
12	1136	80.1	2076	18	US-10-425-114-33866	Sequence 33866, A
13	1136	80.1	2131	20	US-10-425-115-13710	Sequence 13710, A
14	1135	80.0	1388	19	US-10-767-701-13220	Sequence 13220, A
15	1132	79.8	1770	17	US-10-260-238-574	Sequence 574, App
16	1132	79.8	1859	19	US-10-437-963-58337	Sequence 58337, A
17	1127	79.4	1602	9	US-09-938-842A-2304	Sequence 2304, Ap
18	1127	79.4	1602	11	US-09-938-842A-2304	Sequence 2304, Ap
19	1124	79.2	1868	22	US-10-510-871-91	Sequence 91, Appl
20	1115	78.6	2702	19	US-10-437-963-61474	Sequence 61474, A
21	1101	77.6	2054	18	US-10-425-114-32569	Sequence 32569, A
22	1101	77.6	4029	20	US-10-425-115-46503	Sequence 46503, A
23	1084	76.4	2387	19	US-10-437-963-56615	Sequence 56615, A
24	1071	75.5	960	17	US-10-260-238-5509	Sequence 5509, Ap
25	1064.5	75.0	2046	18	US-10-425-114-24849	Sequence 24849, A
26	1064.5	75.0	2068	18	US-10-425-114-32391	Sequence 32391, A
27	1062	74.8	1705	18	US-10-425-114-15775	Sequence 15775, A
28	1048	73.9	2048	20	US-10-425-115-29536	Sequence 29536, A
29	1041	73.4	2325	18	US-10-437-963-84309	Sequence 84309, A
30	1006	70.9	2642	18	US-10-424-599-111533	Sequence 111533, A
31	970	68.4	912	17	US-10-260-238-3517	Sequence 3517, Ap
32	947	66.7	2230	19	US-09-828-313-26	Sequence 26, Appl
33	947	66.7	2230	19	US-10-768-863A-26	Sequence 26, Appl
34	932	65.7	2714	19	US-10-437-963-39308	Sequence 39308, A
35	930	65.5	690	17	US-10-260-238-5765	Sequence 5765, Ap
36	930	65.5	690	22	US-10-481-032A-1186	Sequence 1186, Ap
37	926	65.3	1629	18	US-10-425-114-33660	Sequence 33660, A
38	926	65.3	2642	20	US-10-425-115-156016	Sequence 156016, A
39	921	64.9	1473	17	US-10-260-238-5645	Sequence 5645, Ap
40	916	64.6	1833	11	US-09-938-842A-2334	Sequence 2334, Ap
41	916	64.6	1833	11	US-09-938-842A-2334	Sequence 2334, Ap
42	916	64.6	1839	19	US-10-437-963-37206	Sequence 37206, A
43	914.5	64.4	2530	19	US-10-437-963-31530	Sequence 31530, A
44	910	64.1	2050	18	US-10-425-114-10911	Sequence 10911, A
45	910	64.1	2147	18	US-10-425-114-13091	Sequence 13091, A

ALIGNMENTS

RESULT 1

US-10-243-581B-5
; Sequence 5, Application US/10243581B
; Publication No. US20030219763A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Plant Topoplast Gene Expression Systems
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 00786/386002
; CURRENT APPLICATION NUMBER: US/10243 581B
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/US01/07999
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,074
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: US 08/989,881

;; PRIOR FILING DATE: 1997-12-12
;; PRIOR APPLICATION NUMBER: US 60/032,966
;; PRIOR FILING DATE: 1996-12-13
;; PRIOR APPLICATION NUMBER: US 09/371,338
;; PRIOR FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: US 60/095,938
;; PRIOR FILING DATE: 1998-08-10
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5
;; LENGTH: 1020
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)...(1020)
;; OTHER INFORMATION: N = a, t, c or g
US-10-243-581B-5

Alignment Scores:
Pred. No.: 1,01e-168 Length: 1020
Score: 1419.00 Matches: 274
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-08-989-881-2 (1-274) x US-10-243-581B-5 (1-1020)

Qy 1 MetAlaAsnGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20
Db 97 ATGGCTAATCAAACTCAGATCAGCGAAGTACATCTTAGACGAGAACTCGGTGCGGCG 156
Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 157 GAATTCGGATCAGGTATCTTTGTACAGATAGAGAGACTCGTGAAGCTTTAGCTTGC 216
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Db 217 TCAATCTCCAGAGAAAGCTCCGAACCGCGCTCGATGTGAAGACGTCCTCGTGAAGTC 276
Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db 277 ACGATCATGTCACTTTACCGAAGACCCAAACGTTGTGAACCTTAAGGAGCTTATGAG 336
Qy 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
Db 337 GATAACGAGACCGTGCATCTTTGTGATGGAGCTTTTGTGAAGAGGTGAGCTTTTGTGCGG 396
Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
Db 397 ATTGTTGCAAGAGGACATTTACAGAGCGTGCAGCGGCTACCGTCCGCGAAGCAGATCGCG 456
Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
Db 457 GAAGTTGTGAGGATGTGTCAATGTGTGTATGATAGATAGATTTTGAAGCCCTGAGAA 516
Qy 141 PheLeuPheAlaLeuLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
Db 517 TTCTTGTGTTGCAAGAGGAGAAATTCGCACTTAAGGCTATTGATTGTTGTTATCT 576
Qy 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
Db 577 GTTCTCTTTAAACCTTGAGAGAGGTTTACAGAGATTTGTGAAGTCTCTTATTATATGCT 636
Qy 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
Db 637 CCAGAAGTGTGAAGAGAAATTATGACACAGAGGTTGATGTGTGAGCTGTGGAGTTATC 696
Qy 201 LeuTyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAla 220
Db 697 CTCTACATCTTGTCTTTGTGTTCTCCGTTTGGGCGAGAGACTGAACAAAGGTGTGCT 756

Qy 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGlu 240
Db 757 CTTCGCATCTTGAGGGAGTCTTGTGATTTTAAAGAGAGATCTTGGTCCGAGATATCAGAG 816
Qy 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
Db 817 AGCGCAAGAGACCTTGTGAGCAGATGTTGGAACTGATTAACCTAAGCGTTTGACTGCT 876
Qy 261 GlnGlnValLeuAspHisProTrpIleGlnAsnAlaLysLys 274
Db 877 CAGCAAGTCTTGTGATCACCTTGGATACAGAAATGCAAGAAA 918

RESULT 2

US-09-938-842A-1859
; Sequence 1859, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1859
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1859

Alignment Scores:

Pred. No.: 3,65e-156 Length: 1638
Score: 1322.00 Matches: 253
Percent Similarity: 95.26% Conservative: 8
Best Local Similarity: 92.34% Mismatches: 13
Query Match: 93.16% Indels: 0
DB: 9 Gaps: 0

US-08-989-881-2 (1-274) x US-09-938-842A-1859 (1-1638)

Qy 1 MetAlaAsnGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20
Db 157 ATGAGCAATCAAACTCAGATCAGCGAAGTACATCTTAGTCTGTAATTAGGTGAGGC 216
Qy 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 217 GAATTCGGATCAGTACCTCTGTACTGATCGTGAACCCACGAGCTTTAGCTTGC 276
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Db 277 TCGATTTCAAAGCGAAAGCTTCGAACAGCTGTGATATCGAAGACGCTTCGTCTGAGGTA 336
Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db 337 GCGATTATGTCTACTTTTACTGAGCATCCAAACGATAGTTAAGCTTAAGCTAGTTATGAG 396
Qy 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGlyGluLeuPheGlyArg 100
Db 397 GATACAGCAAGCTGCATCTGTTATGAGCTTTGTGAAGGAGGTGAGCTTTTGTGATCGG 456
Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
Db 457 ATTGTTGCTAGAGGACATTTACAGCGAGCGTGTGCTGCTGAGCTGTTTTCGGAACGATTGCT 516

QY 121 GluValValArgMetCysHisValAenGlyValMetHisArgAspLeuLysProGluAen 140
DB 517 GAGGTGTGATGATGTCTACTATATGAGATTATGCATCGAGATTGAACCTGAGAT 576
QY 141 PheLeuPheAlaAenLysLysGluAenSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
DB 577 TTCTTGTGTCTAATAAAGGAGAGATTCTCCACTAAAGGCTATTGATTTGGCTTGTCT 636
QY 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
DB 637 GTGTCTCTCAACCTCGAGATAAGATTATCAGAGATTGTAGGAAGTCCTGATTATATATGCT 696
QY 181 ProGluValLeuLysArgAspTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
DB 697 CCAGAGTGTGAGAGAGATTATGACAGGGTGTGATGTGGAGTCCCGGAGTATT 756
QY 201 LeuTyrIleLeuLeuCysGlyValProPheTyrPheAlaGluThrGluGlnGlyValAla 220
DB 757 ATCTATATCTGTCTGTGTCTCTCGCTTTCGGCTGAGACTGAACAGGTGTGTCT 816
QY 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGlu 240
DB 817 CTGGCATCTTCGGGGAGTCTTGTGATTTTAAGAGAGACCTTGGCCTCAGATATCAGAG 876
QY 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
DB 877 AGTGCAAGAGCTTGTGAAGCAGATGTTGGATCTGATCCGACTAAGCGGTACTGCT 936
QY 261 GlnGlnValLeuAspHisProTyrIleGlnAenAlaLysLys 274
DB 937 CAGCAAGTGTAGCTCACCCATGGATACAGAAATGCAAGAAA 978

RESULT 3

US-09-938-842A-1859
; Sequence 1859, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krebs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1859
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1859

Alignment Scores:

Pred. No.: 3,65e-156 Length: 1638
Score: 1322.00 Matches: 253
Percent Similarity: 95.26% Conservative: 8
Best Local Similarity: 92.34% Mismatches: 13
Query Match: 93.16% Indels: 0
DB: 11 Gaps: 0

US-08-989-881-2 (1-274) x US-09-938-842A-1859 (1-1638)

QY 1 MetAlaAenGlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGly 20
DB 157 ATGAGCAATCAAACTCAGATCAGCGACAAATACATCTTAGTGTCGTGAATTAGGTCGAGGC 216

QY 21 GluPheGlyIleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
DB 217 GAATTCGGATCATTACTCTGTACTGATCGTGAACCCACGAGAGCTTTAGCTTGCATA 276
QY 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgArgGluVal 60
DB 277 TCGATTTCAAAGCGAAAGCTTCGAACAGCTGTCGATATCGAAGAGCTTCCTCGTGAAGTA 336
QY 61 ThrIleMetSerThrLeuProGluHisProAenValValLysLeuLysAlaThrTyrGlu 80
DB 337 CGCATTTATGTCTTACTTACCTGAGCATCCAAACGCTAGTTAAGCTTAGTTATGAG 396
QY 81 AspAenGluThrValHisLeuValMetGluLeuCysGluGlyGluLeuPheGlyArg 100
DB 397 GATAACGAGAACGCTGCATCTCGTTATGAGCTTTGTGAAGAGAGGTGAGCTTTTGATCGG 456
QY 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
DB 457 ATTGTGTCTAGAGGACATTACAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 516
QY 121 GluValValArgMetCysHisValAenGlyValMetHisArgAspLeuLysProGluAen 140
DB 517 GAGGTGTGATGATGTCTACTTAAATGAGTTATGCATCGAGATTGAAACCTGAGAT 576
QY 141 PheLeuPheAlaAenLysLysGluAenSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
DB 577 TTCTTGTGTCTAATAAAGGAGAGATTCTCCACTAAGGCTATTGATTTGGCTTGTCT 636
QY 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
DB 637 GTGTCTCTCAACCTCGAGATAAGTTTACAGAGATTGTAGGAAGTCCGCTATTATATGCT 696
QY 181 ProGluValLeuLysArgAspTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
DB 697 CCAGAGTGTGAGAGAGATTATGACAGGGTGTGATGTGGAGTCCCGGAGTATT 756
QY 201 LeuTyrIleLeuLeuCysGlyValProPheTyrPheAlaGluThrGluGlnGlyValAla 220
DB 757 ATCTATATCTGTCTGTGTCTCTCGCTTTCGGCTGAGACTGAACAGGTGTGTCT 816
QY 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGlu 240
DB 817 CTGGCATCTTCGGGGAGTCTTGTGATTTTAAGAGAGACCTTGGCCTCAGATATCAGAG 876
QY 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
DB 877 AGTGCAAGAGCTTGTGAAGCAGATGTTGGATCTGATCCGACTAAGCGGTACTGCT 936
QY 261 GlnGlnValLeuAspHisProTyrIleGlnAenAlaLysLys 274
DB 937 CAGCAAGTGTAGCTCACCCATGGATACAGAAATGCAAGAAA 978

RESULT 4

US-10-424-599-37843
; Sequence 37843, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 37843
; LENGTH: 2628
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134173C.1

US-10-424-599-37843

Alignment Scores:

Pred. No.: 5.1e-147 Length: 2628
Score: 1252.00 Matches: 236
Percent Similarity: 92.34% Conservative: 17
Best Local Similarity: 86.13% Mismatches: 21
Query Match: 88.23% Indels: 0
DB: 18 Gaps: 0

US-08-989-881-2 (1-274) x US-10-424-599-37843 (1-2628)

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Qy 1 MetAlaAsnGlnThrGlnIleSerAspLysThrLeuGlyArgGluLeuGlyArgGly 20
Db 194 GTGACGTCAGGAGCGCTCATCGCGCAAGTAGTATAGCGCGGGAGCTAGGTGCTGGC 253
Qy 21 GluPheGlyLeuThrLysCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 254 GAGTTCGGGATAACGTACCTCTGCACGGACCGCGAAGCAAGAGCAGGAGCTCGCGTGAAG 313
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Db 314 TCGATCTCGAAGCGGAAGCTGAGAACCGCATCGACGTGGAGGACGTGCGCGAGAGGTG 373
Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db 374 CGCATCATGTGCGCGGACGCTAACGTGTGTGAAGCTGAAGGCGGACTTACGAG 433
Qy 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
Db 434 GACGAAGAGAACGTTTCATCTCGTTATGGAGCTTTGCGCGCGGGAGCTCTTTGATCGG 493
Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAla 120
Db 494 ATCTCGCGGGGGGCACTACAGCGAGCGTGGCGCGCAAGCTGGCGGAGGACTATTGCT 553
Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
Db 554 GAGTTTGTAGATGTGTACGCCCAATGGTGTATGATCATCGAGACCTTAAGCCAGAGAA 613
Qy 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
Db 614 TTTCTCTTTGGAATAAGAGGAGAAATTCGTTCTCAAGGCTATTGACTTTGGTCTCTGT 673
Qy 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
Db 674 GTGTTTTCATTCAGGGGAGAGTTTGTGGAGATTGTTGGAGTCTCTTACTACATGCGG 733
Qy 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
Db 734 CCGGAGGTTTGAACCGGAATATGGCCAGAGGTTGATGTGGAGTGTGGGGTGATT 793
Qy 201 LeuTyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAla 220
Db 794 CTTTATATTGTTGTGGTGTCTCTCGTTTGGGCGAGGCGCGAGGCGGAGGGGTGGCT 853
Qy 221 LeuAlaIleLeuArgGlyValLeuAspPheLysArgAspProThrSerGlnIleSerGlu 240
Db 854 TTGGCGATCTTGAGAGGTGTGATTGACTTCAAGAGGGAACCTTGGCCACAGATATCGGAG 913
Qy 241 SerAlaLysSerLeuValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
Db 914 AGTGCCAGAGCCTTGTGGCGGAATGTTGGAGCGGATCCTAAAAAGCCCTTGACAGCG 973
Qy 261 GlnGlnValLeuAspHisProThrIleGlnAsnAlaLysLys 274
Db 974 GAACAGGTGCTTGAACATCCCTGCTACAAAATGCAAGAAA 1015
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RESULT 5

US-10-425-114-10952

; Sequence 10952, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovacic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(5313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 10952

; LENGTH: 1787

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: 700989873_FLI

US-10-425-114-10952

Alignment Scores:

Pred. No.: 1.68e-146 Length: 1787
Score: 1246.00 Matches: 235
Percent Similarity: 92.70% Conservative: 19
Best Local Similarity: 85.77% Mismatches: 20
Query Match: 87.81% Indels: 0
DB: 18 Gaps: 0

US-08-989-881-2 (1-274) x US-10-425-114-10952 (1-1787)

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Qy 1 MetAlaAsnGlnThrGlnIleSerAspLysThrIleLeuGlyArgGluLeuGlyArgGly 20
Db 187 GTACGTCAGGAGCGCTCATCGCGCAAGTAGTATAGCGCGGGAGCTAGGTGCTGGC 246
Qy 21 GluPheGlyLeuThrLysCysThrAspArgGluThrArgGluAlaLeuAlaCysLys 40
Db 247 GAGTTCGGGATAACGTACCTCTGCACGGACCGCGAAGCAAGAGCAGGAGCTCGCGTGAAG 306
Qy 41 SerIleSerLysArgLysLeuArgThrAlaValAspValGluAspValArgGluVal 60
Db 307 TCGATCTCGAAGCGGAAGCTGAGAACCGCATCGACGTGGAGGACGTGCGCGGAGAGGTG 366
Qy 61 ThrIleMetSerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGlu 80
Db 367 CGCATCATGTGCGCGTGGCGGACCGCTAAGCTGTGAAGCTGAAGGCGACTTACGAG 426
Qy 81 AspAsnGluThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArg 100
Db 427 GACGAAGAGAACGTTTCATCTCGTTATGGAGCTCTGCGCGCGGGAGCTCTTTCGACCGG 486
Qy 101 IleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAla 120
Db 487 ATCGTCCGCGGGGCACTACAGCGAGCGTGGCGCGCAAGCTGGCGAGGACCATTTGCT 546
Qy 121 GluValValArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsn 140
Db 547 GAGTTTGTAGGATGTGTACGCCAATGTGTATGATCGAGACCTTAAACCTGAGAA 606
Qy 141 PheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSer 160
Db 607 TTTCTCTTTCGGAATAAGAGGAGAAATTCGTTCTCAAGGCTATTGACTTTGAGCTCTCC 666
Qy 161 ValLeuPheLysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAla 180
Db 667 GTGTTTTTCAAGCCAGGGAGAGGTTTTCGAGAGATTGTTGGGAGTCTCTTACTACATGGCG 726
Qy 181 ProGluValLeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIle 200
Db 727 CCGGAGGTTATGNAAGGAATATATGGCCAGAGGTGATGTGTGGAGTGTCTGGGGTGATT 786
Qy 201 LeuTyrIleLeuLeuCysGlyValProPheThrAlaGluThrGluGlnGlyValAla 220
Db 787 CTTTATATTGTTGTGGAGTCTTCGCTTTCGCGAGAGGACGAGGACGAGGAGGCTGGCT 846
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QY 221 LeuAlaIleuArgGlyValLeuAspPheLeuAspProThrSerGlnIleSerGlu 240
DB 847 TTGGCNAATATTGAGGGAGTGATGACTTCAAGAGAAACCGTGGCTCAGATTTCCAGAT 906
QY 241 SerAlaLeuSerLeuValIleGlnMetLeuGluProAspSerThrLysArgLeuThrAla 260
DB 907 ACTGCTAAGAGTCTTGTCGCCAGATGTTGGAGCATGATCCTAAGAAGCGCTTGACGGCT 966

QY 261 GlnGlnValLeuAspHisProThrIleGlnAsnAlaLysLys 274

DB 967 GAACAGGTCTTGAGCATTTCTGGTTACAAAATGCAAGAAA 1008

RESULT 6

US-10-424-599-57457/C
; Sequence 57457, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 57457
; LENGTH: 2126
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_22897C.1
US-10-424-599-57457

Alignment Scores:
Pred. No.: 5,02e-136 Length: 2126
Score: 1164.00 Matches: 217
Percent Similarity: 89.9% Conservative: 24
Best Local Similarity: 80.9% Mismatches: 27
Query Match: 82.0% Indels: 0
DB: 18 Gaps: 0

US-08-989-881-2 (1-274) x US-10-424-599-57457 (1-2126)

QY 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
DB 1694 ATCGAGGACCGGTACTCTGTGACCGCGAGCTCGGGCGCGGAGTTCGGCTGACGTAC 1635
QY 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLeuSerIleSerLysArgLys 46
DB 1634 CTCCTGCATCGACCGCGACACCGCGAGCTGCTCGGTGTGAAGAGCATCTCGAAGAGGA 1575
QY 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66
DB 1574 CTCGGGACAGCGTGGAGCGTGCAGACGTCGCCCGGAGTCCCATCATGCGCCACCTG 1515
QY 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
DB 1514 CCGGAGAGCCCGAGCATCTGTCTCGCGCGAGCTGTGAGGACGACAAATCCCGCTCCAC 1455
QY 87 LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106
DB 1454 CTCGTGATGGAGCTCTGGAGGGCGGGAACCTCTTCGAGCGGATCGTCCCGCGGGGAC 1395
QY 107 TyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys 126
DB 1394 TACACCGAGCGCGCGCGCGCGCTCAGCGGACGATCGTGCAGGTCTGCTGCTGCTGC 1335
QY 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
DB 1334 CACAAGACCGGGGTTCATCCACCGAGACCTCAAGCCGAGAACTTCTTGTTCGCAACAAG 1275

QY 147 LysGluAsnSerAlaLeuIleAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
DB 1274 AAGGAGAATTTCCCTCCCTCAAGCTATTGACITTTGGCTCTCTCATATTCTTCAAGCCAGGT 1215
QY 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
DB 1214 GAGAGTCTCAGAAATTTGTTGGAAGTCCATATTATATGCTCCAGAGTCTCAAGCGG 1155
QY 187 AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysCys 206
DB 1154 AATTATGGACCAAGAAATAGATATATGAGTGCAGGAGTAATTTCTCTACATCTTATTGTGT 1095
QY 207 GlyValProProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
DB 1094 GGTGTTCCCTCAATTTGGCTGAAATCTGAGCAAGAGTTGACAGGCCATTTCTTCAGGA 1035
QY 227 ValLeuAspPheLysArgAspProThrSerGlnIleSerGluSerAlaLysSerLeuVal 246
DB 1034 CTTATAGATTTTAAAGGGAACCATGGCCAGTATTTCTGAAAGTGTCTAAAGCCCTTGT 975
QY 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
DB 974 AGGCAATGTTAGAACCAAGCCCAAGCTTCGATTAACCTGCCAAACAAGTGTCTGAGCAT 915
QY 267 ProThrIleGlnAsnAlaLysLys 274
DB 914 CCTGGATTCAAAATGCTAAGAAG 891

RESULT 7

US-10-437-963-7404
; Sequence 7404, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 7404
; LENGTH: 1978
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14001C.1
US-10-437-963-7404

Alignment Scores:
Pred. No.: 6.21e-135 Length: 1978
Score: 1155.00 Matches: 216
Percent Similarity: 88.81% Conservative: 22
Best Local Similarity: 80.60% Mismatches: 30
Query Match: 81.40% Indels: 0
DB: 19 Gaps: 0

US-08-989-881-2 (1-274) x US-10-437-963-7404 (1-1978)

QY 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
DB 234 ATCCCGCGCGGTACGAGCTGGGCGGAGTTCGGCGCGGAGTTCGGGTTCACCTAC 293
QY 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
DB 294 CTCCTGACGAGCGGAGACCGGGGCGGCTTACGCTGCAAGTCCATCTCTCAAGAAGAAG 353

47	LeuArgThrAlaValAspValGluaspValArgGluValThrIleMetSerThrLeu	56
354	CTCCGCACCGCGCTGGACATGAGGACGTGGCGGAGGTGGACATCATGCCACCTC	413
67	ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis	86
414	CCCAAGCACCCCAACATCGTCAGCTCCGGGACACCTACGAGGACGACAAATGCCGCTCCAC	473
87	LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHis	106
474	CTCGTCATGGAGCTCTGCGAGGCGGGAGGCTCTTCGACCGGATCGTCCCGGGGCCAC	533
107	TyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys	126
534	TACACCGAGCGCGCGCGCGCTGGTGCACCGCCACCATCGTCAGGTCGTGCAGATGTGC	593
127	HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys	146
594	CATAAGCATGGAGTATGCACCGGCACCTCAAAACAGAGAATTTCTGTGTTGCCAAACAAG	653
147	LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly	166
654	AAGGAACCTGCAGCTCTGAAGGCAATTCATTGTGGCCTGTCTGTTTTTTTACC	713
167	GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg	186
714	GAACGGTTCACTGAGATTGCGGAAGCCCTATTATACATGGCTCCTGAGGTGCTAAAGAGA	773
187	AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuCys	206
774	AATTATGGCCCTGAGGTTGATGTTGGAGTCAGAGGTGATCTCTTTATCATCTCTCTTGT	833
207	GlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly	226
834	GGAGTCCCTCCATTTTGGCAGAACTGAACGGGTGTGCTCAGGCAATATCCGTTCT	893
227	ValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuVal	246
894	GTCATTGACTTTCAAGAGAGACCCATGGCCAAAGGCTCTCAGATAAATGCAAGGATCTTGTC	953
247	LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnValLeuAspHis	266
954	AAGGAATGCTCAATCCAGACCCCTAGGGCGGCTAAATGCTCAACAAGTGTTCATCAT	1013
267	ProTrpIleGlnAsnAlaLysLys	274
1014	CTTTGGTTACAGAACATTAAAGAAG	1037

RESULT 8

US-10-425-114-34236
; Sequence 34236, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128

Alignment Scores:	7.18e-134	Length:	2149
Pred. No.:	1147.00	Matches:	215
Score:	89.18%	Conservative:	24
Percent Similarity:	80.22%	Mismatches:	29
Best Local Similarity:	80.83%	Indels:	0
Query Match:	18	Gaps:	0
DB:			
US-08-989-881-2 (1-274) x US-10-425-114-34236 (1-2149)			
Qy	7	I l e s e r A s p l y s t y r i l e L e u G l y A r g G l u L e u G l y A r g G l y l e u P h e G l y l e r t h r T y r	26
Db	458	A T C G C G C G G T A C G A C T C G G C G C G G A G C T C G G C G C G G A G T T C G G G T T A C C T A C	517
Qy	27	L e u C y s T h r A s p A r g L u t h r A r g G l u A l a L e u A l a C y s l y s S e r l e s e r l y s A r g L y s	46
Db	518	C T C T G C A C A C A C G C G C C T C A G G G A G G G C T T G C C T G C A A G T C C A T C T C C A A G A A A G	577
Qy	47	L e u A r g T h r A l a V a l A s p V a l G l u A s p V a l A r g A t g L u V a l T h r l e M e t S e r T h r L e u	66
Db	578	C T C G C A C C G C C T C G A C C T C G A G A C G T G C G C G G A G G T C G A G A T C A T G C C C A C C T C	637
Qy	67	P r o G l u H i s P r o A s n V a l V a l l y s L e u L y s A l a T h r T y r G l u A s p A s n G l u t h r V a l H i s	86
Db	638	C C C A A G C A C C C A A C G T C G T C A C G C T C A G G A C A C G T A C G A G G A C G A C A A T G C C G T G C A C	697
Qy	87	L e u V a l M e t G l u L e u C y s G l u G l y G l y L e u P h e G l y A r g l e V a l l a A r g G l y H i s	106
Db	698	C T C G T C A T G A G C T C T C G A G G C G G T G A G C T T C T C G A C C G C A T C G T G C G C G G G A C A C	757
Qy	107	T y r T h r G l u A r g A l a A l a T h r V a l A l a A r g T h r l e A l e G l u V a l V a l A r g M e t C y s	126
Db	758	T A C A C T G A G G C T C T C C C C C T T G T G T T T A C G C A C T A T T G T T G A G G T C G T C A G A T G T G C	817
Qy	127	H i s V a l A s n G l y V a l M e t H i s A r g A s p L e u L y s P r o G l u A s n P h e L e u P h e A l a A s n L y s	146
Db	818	C A T A A G C A T G G A G T G A T G C A C A G G A T C T C A A A C A G A A A A T T C T G T T T G C A A A C A A G	877
Qy	147	L y s G l u A s n S e r A l a L e u L y s A l a l l e A s p P h e G l y L e u S e r V a l l e u P h e l y s P r o G l y	166
Db	878	A A A G A A T C A G C G C A C T T A A G C C A T T G A T T T T G G C C T G T C T G T A T T T T T C A C A C C A G G C	937
Qy	167	G l u A r g P h e t h r G l u l l e V a l G l y S e r P r o T y r T y r M e t A l a P r o G l u V a l l e u L y s A r g	186
Db	938	G A A C G G T T T C T G A G A T T G T T G G A G T C C T T A T A C T G G C T C C A G A G G T G C T A A G A G A	997
Qy	187	A s n T y r G l y P r o G l u V a l A s p V a l T r p S e r A l a G l y V a l l e u T y r l e L e u L e u C y s	206
Db	998	A A C T A T G G C C A G A G T T G A T G T T T G G A G T G C A G G A G T G A T T C T G T A C A T T C T C T T T G T	1057
Qy	207	G l y V a l P r o P h e t r p A l a G l u t h r G l u G l n G l y V a l A l e u A l a l l e L e u A r g G l y	226
Db	1058	G G T G T C C C C C A T T C T G G C A G A A C C G A A C A G G G T T G C T C A G G C A A T C A T T C G A T C T	1117
Qy	227	V a l l e u A s p P h e l y s A r g A s p P r o T r p S e r G l n l e s e r G l u S e r A l a l y s S e r L e u V a l	246
Db	1118	G T C A T T G A T T T C A A A G A G A T C C A T G C C A A G G G T G T C T G A T A A C C C A A A G A C C T T G T C	1177
Qy	247	L y s G l u M e t L e u G l u P r o A s p S e r T h r l y s A r g L e u T h r A l e G l n G l n V a l l e u A s p H i s	266
Db	1178	A G A A A A T G T G A A T C C G A C C C A A A A C A C A G A T T G A C A G C T C A C C A A G T G T T G T G C A C	1237
Qy	267	P r o T r p l e G l n A s n A l a l y s l y s	274
Db	1238	C C A T G G T T G C A A C A C A T T A A G A A G	1261

RESULT 9

US-10-425-114-28411
; Sequence 28411, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 28411
; LENGTH: 2244
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4757-010-H10_FLI
US-10-425-114-28411

Alignment Scores:
Pred. No.: 2,45e-133 Length: 2244
Score: 1143.00 Matches: 215
Percent Similarity: 88.81% Conservative: 23
Best Local Similarity: 80.22% Mismatches: 30
Query Match: 80.55% Indels: 0
DB: 18 Gaps: 0

US-08-989-881-2 (1-274) x US-10-425-114-28411 (1-2244)
Qy 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
Db 541 ATCGCGCGCGGTACGAGCTCGCGCGGAGCTCGCGCGGAGTTCGGGGTTACCTAC 600
Qy 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerIleArgLys 46
Db 601 CTCTGCACAGACCGTGCCTCAGGGGAGCGCTGCGCTGCAAGTCTATCTCCAAGAAGAAG 660
Qy 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66
Db 661 CTCGACACCGCGTGCAGCTCGAGGACGTGCGCGGAGGTGGAGATCATGCGCCACCTC 720
Qy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db 721 CCCAAGCACCCCAAGCTGTCACGCTCAGGGACAGTACGAGGACGACAAATGCCGTGCAC 780
Qy 87 LeuValMetGluLeuLysGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106
Db 781 CTCGTCATGAGCTGCGAGGCGGTGAGCTCTTCGACCGCATCGTGGCGCGGGGACAC 840
Qy 107 TyrThrGluArgAlaAlaThrValAlaThrIleAlaGluValValArgMetCys 126
Db 841 TACACTGAGCGTGTGCGCGCTTGTGCTTACGCACTATCGTGGTGTGTCGATGTGC 900
Qy 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
Db 901 CATAAGCATGAGTGATGCACAGGATCTCAACACCAAGAAATTTTGTGTTGCAACCAAG 960
Qy 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
Db 961 AAAGAAATCAGCGGCACCTTAAGGCCATTGATTTGGCCCTGTCTGTATTTTCACTCCAGGC 1020
Qy 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
Db 1021 GAACGGTTTCTGAGATTGTTGGAAGTCTTATTACATGGCTCGAGAGTGATCTGTACATCTCTTGT 1140
Qy 187 AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysCys 206
Db 1081 AACTATGCCCCAGAGTTGATGTTGGAGTGCAGAGTGATCTGTACATCTCTTGT 1140
Qy 207 GlyValProProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
Db 1141 GGTGTCCCCCATTTCTGGGCAGAAACGGAACAGGGTGTGTGCTCAGGCAATCATTCGATCT 1200

227 ValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuVal 246
1201 GTCAATTGATTTCAAAAGAGATCCATGGCCAAAGGTGTCTGATAACGCCAAACACCTTGT 1260
247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
1261 AGAGGAATGCTGAATCCGGACCCCAAAACGACGATTGACAGCTCACCAAGTCTTGGTCAC 1320
267 ProTrpIleGlnAsnAlaLysLys 274
1321 CCATGGTTGCAGAACATTAAAGAAG 1344

RESULT 10
US-10-425-115-28928
; Sequence 28928, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 28928
; LENGTH: 2298
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_126393C.1
US-10-425-115-28928

Alignment Scores:
Pred. No.: 2,54e-133 Length: 2298
Score: 1143.00 Matches: 215
Percent Similarity: 88.81% Conservative: 23
Best Local Similarity: 80.22% Mismatches: 30
Query Match: 80.55% Indels: 0
DB: 20 Gaps: 0

US-08-989-881-2 (1-274) x US-10-425-115-28928 (1-2298)
Qy 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
Db 546 ATCGCGCGCGGTACGAGCTCGCGCGGAGCTCGCGCGGAGTTCGGGGTTACCTAC 605
Qy 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerIleArgLys 46
Db 606 CTCTGCACAGACCGCGCTCAGGGGAGCGCTGCGCTGCAAGTCCATCTCCAAGAAGAAG 665
Qy 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66
Db 666 CTCGACACCGCGTGCAGCTCGAGGACGTGCGCGGAGGTGGAGATCATGCGCCACCTC 725
Qy 67 ProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
Db 726 CCCAAGCACCCCAAGCTGTCACGCTCAGGACACGTCAGGAGGACGACAAATGCCGTGCAC 785
Qy 87 LeuValMetGluLeuLysGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106
Db 786 CTCGTCATGAGCTGTCGAGGCGGTGAGCTCTTTCAGCGCATCTGTCGCGCGGGGACAC 845
Qy 107 TyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMetCys 126
Db 846 TACACTGAGCGTGTGCGCGCTTGTGCTTACGCACTATCGTGGTGTGTCGTCAGATGTGC 905
Qy 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
Db 906 CATAAGCATGAGTGATGCACAGGATCTCAACACCAAGAAATTTTCTTGTGTTGCAACCAAG 965
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QY 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
 DB 966 AAAGAAATCAGCGGCACCTAAGGCATTTGAGCTGCTGTTATTTTTCACACCGGC 1025
 QY 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
 DB 1026 GAACGGTTTCTGAGATTGTTGGAGTCCCTATTACATGGCTCCAGAGGTGCTAAAGAGA 1085
 QY 187 AsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeuTyrIleLeuLysCys 206
 DB 1086 AACTATGGCCACAGAGTGTATGTTGGAGTGCAGAGTGTCTGTACATCTCTCTTTGT 1145
 QY 207 GlyValProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
 DB 1146 GGTGTCCCCCATCTCGGCAGAACCGAAGAGGGTGTGCTCAGCAATCAATTCGATCT 1205
 QY 227 ValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSerAlaLysSerLeuVal 246
 DB 1206 GTATTGATTCAAGAGATCCATGGCCAGGGTGTCTGTAACGCCAAGACCTTGTCT 1265
 QY 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
 DB 1266 AGAGGAATGCTGAATCGGACCGACCCCAACAGCAGATTGACAGTCCACCAAGTGTGTGTCTAC 1325
 QY 267 ProTyrPheGlnAsnAlaLysLys 274
 DB 1326 CCATGGTTGCAGAACATTAAAGAG 1349

RESULT 11

US-10-425-114-24006
 ; Sequence 24006, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 24006
 ; LENGTH: 1974
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3606-058-A10_FLI
 US-10-425-114-24006

Alignment Scores:
 Pred. No.: 1-56e-132 Length: 1974
 Score: 1136.00 Matches: 212
 Percent Similarity: 88.81% Conservative: 26
 Best Local Similarity: 79.10% Mismatches: 30
 Query Match: 80.06% Indels: 0
 DB: 18 Gaps: 0

US-08-989-881-2 (1-274) x US-10-425-114-24006 (1-1974)

QY 7 IleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThrTyr 26
 DB 368 ATCGACGACAAGTACGTCCTGGACAGGAGTCGCGCGGGAGTTCGGGGTCCACGTAC 427
 QY 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys 46
 DB 428 CTGTGTATGATCGGACACAGAGCTGCTCCCTCCCAAGTCCATCTCCAGCGCAAG 487
 QY 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66

DB 488 CTGCGGACGCGCGTGCACGTGGAGGAGCTGCGCGGGAGGTGGCCATCATGCGCCACCTG 547
 QY 67 ProGluHiProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis 86
 DB 548 CCCAAGAGCGCCAGCGCTGCTCCCTCGCGGAGGCGTGGCAGGACGACGCGCGCTCCAC 607
 QY 87 LeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaAspGlyHis 106
 DB 608 CTGCTCATGAGCTCTGCGAGGCGCGGAGCTCTTCGACCGCATCTGCGCGCGGGGCCAC 667
 QY 107 TyrThrGluArgAlaAlaThrValAlaIleArgThrIleAlaGluValValAlaArgMetCys 126
 DB 668 TACACCGAGCGCGCCCGCCAGTGTCCACCGCACCATCTCTCGAGGTGCTCCAGCTGTC 727
 QY 127 HisValAsnGlyValMethHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
 DB 728 CACCGCACGGCGCTCATCCACCGCGACCTCAAGCGCGAGAACTTCCTCTTCGCCAATAAG 787
 QY 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
 DB 788 AAGGAGAACTCGCGCTCAAGGCCATCGACTTCGGTCTCTCCATCTCTTCAAGCCTGGT 847
 QY 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
 DB 848 GAAAGCTTTTCAGAAATTTGCGGAGCCCTATTACATGGCTCCTGAAAGTATTGAAGAGA 907
 QY 187 AsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeuTyrIleLeuLysCys 206
 DB 908 AACTATGGCCACGAAATACACATATGAGGTGCGGAGTTATCTGTATATTTTATTATGT 967
 QY 207 GlyValProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
 DB 968 GGAGTCCCTCCATTTTGGGCTGAGACTGAACAAGGGGTGGCGGAGGTATCTTCGTGGA 1027
 QY 227 ValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSerAlaLysSerLeuVal 246
 DB 1028 AATATCGATTTTAAAGCGGAAACCTCGCTTAATGTTTCGAAAAATGCAAAAGATTAGTT 1087
 QY 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
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 QY 267 ProTyrPheGlnAsnAlaLysLys 274
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RESULT 12

US-10-425-114-33866
 ; Sequence 33866, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 33866
 ; LENGTH: 2076
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-ZMFLMO17179A04_FLI
 US-10-425-114-33866

Alignment Scores:
 Pred. No.: 1-68e-132 Length: 2076

Score:	1136.00	Matches:	212
Percent Similarity:	88.81%	Conservative:	36
Best Local Similarity:	79.10%	Mismatches:	20
Query Match:	80.06%	Indels:	0
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US-08-989-881-2 (1-274) x US-10-425-114-33866 (1-2076)

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Qy	27	LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLys	46
Db	397	CTGTGTATGGATCGGGACCAAGAGAGCTGCTCGCTTGCAGTCCATCTCCAGCGCAAG	456
Qy	47	LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu	66
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Qy	67	ProGluHisProAsnValLysLeuLysAlaThrTyrGluAspAsnGluThrValHis	86
Db	517	CCCAAGAGCCCCAGCGTCGTCTCCCTCGGGAGCGTCGCCAGGACGACGGCGCGTCCAC	576
Qy	87	LeuValMetGluLeuCysGluGlyGluLeuPheGlyArgIleValAlaArgGlyHis	106
Db	577	CTCGTCATGGAGCTCTCGAGGGCGGCGAGCTCTTCGACCGCATCGTCGCGGGGGCCAC	636
Qy	107	TyrThrGluArgAlaAlaIaThrValAlaAargThrIleAlaGluValValaArgMetCys	126
Db	637	TACACCGAGCGCGCGCGCGAGTGTACCGCACCATCTCTCGAGGTCTGCCAGCTCTGC	696
Qy	127	HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys	146
Db	697	CACCGCACGGCGTCACTCCACCGCGACTCAAGCCGGAGAACTCTCTTCGCCCAATAAG	756
Qy	147	LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly	166
Db	757	AAGGAGAACTCGCGCTCAAGGCCATCGACTTCGGTCTCTCCATCTTCTTCAAGCCTGGT	816
Qy	167	GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg	186
Db	817	GAAAGATTTTCAGAAATTTGTGGGAAGCCCTATTACATGGCTCTCGAAGTATTGGAAGAGA	876
Qy	187	AsnTyrGlyProGluValAspValTribSerAlaGlyValIleLeuTyrIleLeuLeuCys	206
Db	877	AACTATGGCGCAGAAATAGACATATGAGGTGCGGAGTTATCTCTGTATATTTATTATGT	936
Qy	207	GlyValProProPheTribAlaGluThrGluGlnIlyValAlaLeuAlaIleLeuArgGly	226
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Qy	227	ValLeuAspPheLysArgAspProTribSerClnIleSerGluSerAlaLysSerLeuVal	246
Db	997	AATATCATGATTTTAAGCCGGAAACCTCGGCCCTAAATGTTTCGGAATAATGCAAAAGATTTAGTT	1056
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Db	1117	CATTGGCTTCAAAATGCAAGAAG	1140

RESULT 13

US-104-425-115-13710
; Sequence 13710, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei


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QY 47 LeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThrLeu 66
Db |||||
QY 337 CTGAGACGGCGTTCACGTGGAGGACGTGCGCGGAGGTGCCATCATGCCACCTC 396
Db |||||
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QY 397 CCCAAGAGCCCGACGATCGTGTGCTGCGGAGGCGTGCAGGACGAGGCGCGTGCAC 456
Db |||||
QY 87 LeuValMetClnLeuGlyGluGlyGluLeuPheGlyArgIleValAlaArgGlyHis 106
Db |||||
QY 457 CTCGTATGGAGCTCTGCGAAGCGGGAGCTCTTCAGCCGATCGTGCAGCGGGGCCAC 516
Db |||||
QY 107 TyrThrGluArgAlaAlaThrValAlaThrIleAlaGluValValArgMetCys 126
Db |||||
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Db |||||
QY 127 HisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLys 146
Db |||||
QY 577 CACCGCCAGCGCGTTATCCACCGGACCTCAAGCCGAGAACTTCCTCTTCGCCAACAG 636
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QY 147 LysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGly 166
Db |||||
QY 637 AAGGAACTCGCGCTCAAGGCCATCGATTCGGGCTCTCCATCTTCTCAAGCCCGGT 696
Db |||||
QY 167 GluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArg 186
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Db |||||
QY 187 AsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysCys 206
Db |||||
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Db |||||
QY 207 GlyValProProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGly 226
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Db |||||
QY 227 ValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuVal 246
Db |||||
QY 877 AATATCGATTTCAACCGGNACCTGCGCAAAATGTTTCAGAAAATGCTAAAGATTGGTT 936
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QY 247 LysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHis 266
Db |||||
QY 937 CGACGCATGTTGGAGCTGATCCAAAACCTCAGGTAACTGCAAAAGCAAGTTCTTGAACAT 996
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QY 997 CCATGGCTTCAAAATGCTAAGAAA 1020
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Search completed: October 14, 2005, 20:55:30
Job time : 773 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 14, 2005, 18:23:22 ; Search time 3512 seconds
(without alignments)
2969.707 Million cell updates/sec

Title: US-08-989-881-2
Perfect score: 1419
Sequence: 1 MANQTQSDKYLRELGRG.....TKRLTAQVLDHPWQNAKK 274

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_epool/US08989881/runat_14102005_112734_5205/app_query.fasta_1.455
-DB=EST -QFMT=fastcap -SUFFI=1 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08989881 @CGN 1_1_4352 @runat_14102005_112734_5205 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-FEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.*

```
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gest1.*
9: gb_gest2.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1141	80.4	1963	CNSOA743	BX822805 Arabidops
2	1132	79.8	1770	CL960178	CL960178 OsIFCC003
3	1116	78.6	2037	CNSOA1F3	BX830195 Arabidops
4	1102	77.7	833	BE641223	BE641223 Cr12.2_K0
5	1094	77.1	1964	CNSOA4Q0L	BX824980 Arabidops
6	1046	73.7	1840	CNSOA93C	BX821136 Arabidops
7	1042	73.4	768	BU003544	BU003544 QGG35J03
8	1011	71.2	721	CK250764	CK250764 EST734401
9	1005	70.8	711	CA264357	CA264357 SCQGLB204

10	1004	70.8	982	7	CK281626
11	950	66.9	889	7	CK297575
12	945	66.6	864	6	CB894498
13	943	66.5	688	6	CA266323
14	940	66.2	679	5	BQ148394
15	938.5	66.1	914	7	CV470355
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17	935	65.9	659	2	AW685409
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23	912	64.3	642	7	CN897553
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26	907	63.9	778	7	CF394637
27	907	63.9	1719	9	CL969653
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40	880	62.0	2298	3	AY109401
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42	877	61.8	903	7	CK271484
43	876	61.7	957	7	CK255123
44	875	61.7	612	4	BJ479365
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ALIGNMENTS

RESULT 1
LOCUS CNSOA743 1963 bp mRNA linear HTC 06-FEB-2004
DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTF865ZB09 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
ACCESSION BX822805 GI:42466038
VERSION BX822805
KEYWORDS HTC; GSLT cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 1963)
AUTHORS Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissbach, J. and Salanoubat, M.
TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1963)
AUTHORS Direct Submission
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

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CB894498	EST647290
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CV470355	43200.1 C
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AW685409	NF029A07N
BX833090	BX833090
CK289074	EST751796
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CO082724	GR_Ea47H
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 QY 127 HisValAsnGlyValMetHisArgAspLeuYsProGluAsnPheLeuPheAlaAsnLys 146
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 Db 697 GAGAAATTTCTCAAAATTGCGAAGCCCATATTACATGCTCCAGAGTATTGAAGAGA 756
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 QY 267 ProTyrIleGlnAsnAlaLysLys 274
 Db 997 CCATGGCTTCAAAATGCTAAGAAA 1020

CNS0A1F3 2037 bp mRNA linear HTC 06-FEB-2004
 Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 GSLTFB65ZE02 of flowers and buds of strain col-0 of Arabidopsis
 thaliana (thale cress).
 BX830195
 EX830195.1 GI:42458643
 HTC; GSLT cDNA.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2037)
 Castell, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
 Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
 Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
 Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
 A Combined Approach to Evaluate and Improve Arabidopsis Genome
 Annotation
 Unpublished
 2 (bases 1 to 2037)
 Genoscope.
 Direct Submission
 Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)

COMMENT The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castelli
 V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
 Schachter V., Weissenbach J., Salanoubat M.
 URGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich Information center for Protein
 Sequences). 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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 /gene="At5g12480"

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 Score: 1116.00 Matches: 209.
 Percent Similarity: 87.63% Conservative: 26
 Best Local Similarity: 77.99% Mismatches: 33
 Query Match: 78.65% Indels: 0
 DB: 3 Gaps: 0

US-08-989-881-2 (1-274) x CNS0A1F3 (1-2037)
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 Db 369 ATATCTCTCGCATGATGATCTTGGAGCTGAGTGTGTCGAGGCGAGTTTGGTATTAATTAC 428
 QY 27 LeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerLysArgLys 46
 Db 429 TTGTGTACTGATAAGAACTGGTGAGAAGTATGCTGCAAGTCCATATCTAAGAAGAAG 488
 QY 47 LeuArgThrAlaValAspValGluAspValArgArgGluValThrIleMetSerThrLeu 66
 Db 489 CTGAGAACGACGATGATATAGAGGATGTTAGGAGGAGGTTGAGATTATGAAGCATATG 548
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 Db 849 GAGCAGTTTAAATGAGATTGTTGGAAGTCTTTATTACATGGCACCCGAGGTCTCGCGCA 908
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||||| 1149 ACTGGATAGTCAATGCANAGAG 1172
Db

RESULT 4
BE641223 833 bp mRNA linear EST 01-SEP-2000
LOCUS
DEFINITION Cui2_2_K07.SP6 Ceratopteris Spore Library Ceratopteris richardii
cDNA_clone_Cui2_2_K07_5', mRNA sequence..
ACCESSION BE641223
VERSION BE641223.1 GI:9958885
KEYWORDS EST.
SOURCE Ceratopteris richardii
ORGANISM Ceratopteris richardii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Moniliformopses; Filicophyta; Filicopsida; Filicales; Pteridaceae;
Ceratopteris.
REFERENCE 1 (bases 1 to 833)
AUTHORS Chatterjee,A., San Miguel,P., Stout,S.C., Banks,J. and Roux,S.J.
TITLE Expressed sequence tags of cDNA clones from a C. richardii library
JOURNAL Unpublished (2000)
COMMENT Contact: Roux SJ
Section of Molecular Cell and Developmental Biology
University of Texas
Biology Building, Room 16, Austin, TX 78712, USA
Tel: 512 471 4238
Fax: 512 232 3402
Email: sroux@uts.cc.utexas.edu
Plate: Cui2_2 row: K column: 07
Seq primer: SP6.
Location/Qualifiers
source 1..833
/organism="Ceratopteris richardii"
/mol_type="mRNA"
/cultivar="Brogan"
/db_xref="taxon:49495"
/clone="Cui2_2_K07"
/tissue_type="Gametophyte"
/cell_type="Spore"
/dev_stage="20 hours after germination initiation"
/clone_lib="Ceratopteris Spore Library"
/note="vector: pCMVSPORT6; EST sequence from cDNA library.
cDNA library constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after
their germination had been initiated by white light."

ORIGIN
Alignment Scores: 2.92e-120 Length: 833
Pred. No.: 1102.00 Matches: 206
Score: 88.08% Conservative: 23
Percent Similarity: 79.23% Mismatches: 31
Best Local Similarity: 77.66% Indels: 0
Query Match: 2 Gaps: 0
DB:

US-08-989-881-2 (1-274) x BE641223 (1-833)

Qy 15 ArgGluLeuGlyArgGlyGluPheGlyLeuThrTyrLeuCysThrAspArgGluThrArg 34

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```

... 6 AAGAGACTTGGTCTGTGTGAATTTGGCATCACCTTACTTATGTCAGATCGGAGACTGAC 65
Db
||||| 35 GluAlaLeuAlaCysLysSerIleSerLysArgLysLeuArgThrAlaValAspValGlu 54
Qy
||||| 66 GAAGTCTAGCATGTAATCTATTCTTAAGGGAAGCTTAGGACACCCATGACATTGAA 125
Db
||||| 55 AspValArgArgGluValThrIleMetSerThrLeuProGluHisProAsnValValLys 74
Qy
||||| 126 GATGTTTCCGAAGAGAGGTGGATATATGAGACATCTTCTTAACATCCAAACATTTGTGACT 185
Db
||||| 75 LeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGluLeuCysGluGly 94
Qy
||||| 186 TTGAAGGGGTGATGAGGATGAGATGCAATCTTGTCTATGGAACCTATGTGAAGGT 245
Db
||||| 95 GlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArgAlaAlaThr 114
Qy
||||| 246 GGTGAATTTTCGATCGCATTTGTAGCAAGAGGTCACTACAGCGAGAGAGCTGCAGTGGC 305
Db
||||| 115 ValAlaArgThrIleAlaGluValValArgMetCysHisValAsnGlyValMetHisArg 134
Qy
||||| 306 GTCATGCGTACCATTTCTTGAAGTTGTACAGTTTGCATAGGCATGGTGTCTATGCCCGC 365
Db
||||| 135 AspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAla 154
Qy
||||| 366 GACCTTAAGCCAGAAAATTTCTGTTTGCANAAAGAAAATTCGCCCTTAAAGCT 425
Db
||||| 155 IleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPheThrGluIleValGly 174
Qy
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Db
||||| 175 SerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyProGluValAspVal 194
Qy
||||| 486 AGTCCATACCTATATGTCACCTGAGGTACTGAAAGAAGTTATGGCCAGAGTTGATATA 545
Db
||||| 195 TrpSerAlaGlyValIleLeuTyrIleLeuLysCysGlyValProPheTTPAlaGlu 214
Qy
||||| 546 TGGAGTGCAGAGGTATATCTTTATCATCTTTTATGCGGAGTCCCCCTTTTGGGCTGAG 605
Db
||||| 215 ThrGluGlnGlyValAlaLeuAlaLeuArgGlyValLeuAspPheLysArgAspPro 234
Qy
||||| 606 ACCGAACAATTAGTAGCCAGGCCATCTTACGTGGAAATGTGGACTTCAACAGAGATCCT 665
Db
||||| 235 TrpSerGlnIleSerGluSerAlaLysSerLeuValLysGlnMetLeuGluProAspSer 254
Qy
||||| 666 TGCCCAAAATGTTTCAGAAAATGCTAAAGCGCTAGTCGCGCAAAATGCTTGGACCCAGATCCA 725
Db
||||| 255 ThrLysArgLeuThrAlaGlnGlnValLeuAspPheProTTPLeuGlnAsnAlaLysLys 274
Qy
||||| 726 AGCCAAAGATTGACAGCTCAACCAAGTCTTGATCATCTTGGTGGCTTGTGAATGCAAGAAA 785
Db

CNS0A4QL 1964 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTGH872B07 of Hormone Treated Callus of strain col-0 of
Arabidopsis thaliana (thale cress).
BX824980
BX824980.1 GI:42462449
HTC; GSLT cDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopses.
1 (bases 1 to 1964)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Comparisons and 'Full-length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
JOURNAL

```


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Pred. No.:	4.21e-113	Length:	1840
Score:	1046.00	Matches:	193
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Best Local Similarity:	71.75%	Mismatches:	37
Query Match:	73.71%	Indels:	1
DB:	3	Gaps:	0
US-08-989-881-2 (1-274) x CNS0A93C (1-1840)			
Qy	6	GlnileSerAspLysThrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThr	25
Db	89	GAGATCAAGCAGAAATATAAATTAGTCTGAGTTAGTTCGAGGAGAGTTTCGGTGTCACG	148
Qy	26	TyrLeuCyThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArg	45
Db	149	TATCTGTGCACCGAGATCGAGACCGAGAGATTTTCTCATGCAAAATCAATCTTAAAGAAG	208
Qy	46	LysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMetSerThr	65
Db	209	AAGCTGAAACGTCGATTGATATAGAGAGCTTAAGAGAGAAAGTTGAGATCATGAGGCAA	268
Qy	66	LeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrVal	85
Db	269	ATGCTTGAACATCTTAATTTGTTACTTTGAAAGAGACTTATGAGGATGATAAGCTGTG	328
Qy	86	HisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGly	105
Db	329	CATTGTGTTAAGAGCTTTGTGAAGCGGTGACCTTTTCATAGGATTTGTTGTAGAGGG	388
Qy	106	HisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMet	125
Db	389	CATTATACGAGAGAGCTGCTGCTTCGGTTATTAAACAGATCATCGAGGTTGTCAGATG	448
Qy	126	CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn	145
Db	449	TGTCATAAGCATGGAGTAATGCACAGAGATTTAAACCTGAGAACTTCTTTGTTGCAAC	508
Qy	146	LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro	165
Db	509	AAGAAGAACTGCATCTTTTAAAGGCTATTAAATTAAGTCTCTCTGTATACATTAACCA	568
Qy	166	GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys	185
Db	569	GGCGAGAAATTTAACGAATTTCTTGGAGTCCCTTACTACATGGCTCCTGAAGTATTAAAG	628
Qy	186	ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu	205
Db	629	AGAGATCATGCAACAGACATTCACATTTGAGCGCAGGAGTGATTTCTTACATATTGCTC	688
Qy	206	CysGlyValProPheTrp-AlaGluThrGluGlnGlyValAlaLeuAlaIleLeuAr	225
Db	689	TGTGGTGTCTCACCTTTTCTCGGCAGAAACCGAATGAGTGCAGAAAGCAATTTCTTAA	748
Qy	225	gGlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLe	245
Db	749	ATCTGTAATTAACITTAAGAGACCCCTGGCTTAAAGTTTCTGTAATGCAAAAGATCT	808
Qy	245	uValLysGlnMetLeuGluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAs	265
Db	809	GATCAAAAGATGCTTCATCCTCATGCCAAGGCGTCGCTTAACCTGCTCAACCAAGTGCTTGA	868
Qy	265	pHisProTrpIleGlnAsnAlaLys	273
Db	869	TCATCCGTGGATACAGAATCGTAAG	893
RESULT 7			
BU003544			
LOCUS			
DEFINITION			
QGG35J03.yg.ab1 QG_EFGHU lettuce serriola Lactuca sativa cDNA clone			
QGG35J03, mRNA sequence.			
ACCESSION			
BU003544			
VERSION			
BU003544.1			
KEYWORDS			
EST.			
SOURCE			
Lactuca sativa			
ORGANISM			
Lactuca sativa			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;			
Cichorieae; Lactuca.			
1 (bases 1 to 768)			
REFERENCE			
AUTHORS			
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesberg, L.,			
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,			
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,			
Lai, Z., Church, S., Jackson, L. and Bradford, K.			
Lettuce and Sunflower ESTs from the Compositae Genome Project			
http://compgenomics.ucdavis.edu/			
JOURNAL			
COMMENT			
Unpublished (2002)			
Contact: Alexander Kozik [R.W.Michelmore]			
Department of Vegetable Crops, R.W.Michelmore Lab			
University of California at Davis (UCD)			
Asmundson Hall, UCD, Davis, CA 95616, USA			
Tel: 1-(530)-742-1742			
Fax: 1-(530)-752-9659			
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]			
belongs to contig QG_CA_Contig5725, see http://cgpdb.ucdavis.edu/			
for details.			
Plate: QGG35 row: J column: 03.			
FEATURES			
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1..768			
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/cultivar="L.serriola"			
/db_xref="taxon:4236"			
/clone="QGG35J03"			
/lab_host="E.coli"			
/clone_lib="QG_EFGHU lettuce serriola"			
/note="Vector: pBRCN4SFIAB; The library was constructed			
from 10 different sources of RNA from a single genotype.			
Separate cDNAs were generated using primers that			
incorporated unique 5' and 3' tags to distinguish each			
source of RNA. cDNAs were then pooled, size-fractionated,			
directionally cloned into a custom medium-copy vector and			
transformations made with four size classes to minimize			
size bias. Details of each source of RNA and library			
construction can be obtained at http://cgpdb.ucdavis.edu/			
TAG_TISSUE=germinating seeds			
TAG_LIB=QG_EFGHU lettuce serriola			
TAG_SEQ=TCGTGCGGG			
ORIGIN			
Alignment Scores:			
Pred. No.: 3.64e-113			
Score: 1042.00			
Percent Similarity: 89.17%			
Best Local Similarity: 80.00%			
Query Match: 73.43%			
DB: 5			
US-08-989-881-2 (1-274) x BU003544 (1-768)			
Qy	6	GlnileSerAspLysThrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThr	25
Db	49	GAGATTCAGGAAACTTATGTTCTTGGTAAGCAATTTGGCAGAGAGAAATTTGGCATTA	108
Qy	26	TyrLeuCyThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArg	45
Db	109	TATATGTGTACAGATAAGTCAACTGGTGAATTTTGTGTTGTAATCGATATCCAAAG	168
Qy	46	LysLeuArgThrAlaValAspValGluArgGluValThrIleMetSerThr	65

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Db      169  AGTTGAGGACTAGGTTGATATCGAGGATTTAGAGAGAGATTGAGATCATGGAGCAT 228
Qy      66  LeuProGluHisProAsnValVallysLeuLysAlaThrTyrGluAspAsnGluThrVal 85
Db      229  ATGCCTACTCACCTAATATCGTCCTTGAAGACACATACAGCAATGATAGTGTGTT 288
Qy      86  HisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGly 105
Db      289  CATTGTGTCATGGAGCTGTGCGAGGAGGAGAAATTAATCGATCGGATTTGTCCAGAGGC 348
Qy      106  HisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValValArgMet 125
Db      349  CACTACACGAGAGAGCCCGCGGCTCACAGGACCATCTCGAAGTCATTAGATG 408
Qy      126  CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsn 145
Db      409  TGCCCAACAGCATGTTTATGTCATCGTATCTTAACCCGMAAATTTTGTGTGCAAC 468
Qy      146  LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro 165
Db      469  AAGAAGAACACAGCAGCTTTAAAGCTATGTGATTTTGGGTATPCCGTTTCTTCAAACCA 528
Qy      166  GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys 185
Db      529  GCGGAGAGTTTAAACGAATTTAGGCAGTCCATACATGATGGCTCTGAGGTCTTAA 588
Qy      186  ArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIleLeu 205
Db      589  AGAAACTATGGCCCAAGTTGACGTATGCAGTGCAGGGGTAATCTTGATACATATTGCTT 648
Qy      206  CysGlyValProPheThrAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArg 225
Db      649  TGTGAGTCCCTCCATTTTGGGAGAACTGACAGAGGAGTTGCACAAACAATTTATCGA 708
Qy      226  GlyValLeuAspPheLysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeu 245
Db      709  TCAGTTGTAGATTTTAAAGGATCCATGGGCCAGGATCTGATGCACCTAAAGATCTT 768

RESULT 8
CK250764 721 bp mRNA linear EST 30-JUL-2004
LOCUS EST734401 potato callus cDNA library, normalized and full-length
DEFINITION Solanum tuberosum cDNA clone POCB139 5' end, mRNA sequence.
ACCESSION CK250764
VERSION CK250764.1 GI:39803147
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum

REFERENCE
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE Generation of ESTs from potato callus tissue
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST734402
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1. .721
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCB139"
/tissue_type="callus"
/lab_host="DH10B-TonA"

FEATURES
source

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/clone_lib="potato callus cDNA library, normalized and
full_length"
/note="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."

ORIGIN
Alignment Scores:
Pred. No.: 1,648-109 Length: 721
Score: 1011.00 Matches: 188
Percent Similarity: 96.67% Conservative: 15
Best Local Similarity: 89.53% Mismatches: 7
Query Match: 71.25% Indels: 0
DB: 7 Gaps: 0

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US-08-989-881-2 (1-274) x CK250764 (1-721)
Qy      4  GlnThrGlnIleSerAspLysTyrIleLeuGlyValArgGluLeuGlyArgGlyGluPheGly 23
Db      90  AAAACATGCATATCTGACAAATACATCTTAGACACGAGAACTGGGTGGGGCGAATTTGGA 149
Qy      24  IleThrTyrLeuCysThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSer 43
Db      150  GTGACTTACCTTTGACCCGACAGGAGACCCGAGATGCCCTTGTCTTCAAATCTATTCA 209
Qy      44  LysArgLysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMet 63
Db      210  AAGAAGAAGCTCCGAACAGCTGTGATATCGAAGATGTGAGAGAGAGTGTGCTATTATG 269
Qy      64  SerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGlu 83
Db      270  TCAGCCCTCTCTGATCACCCTAATTTGTGAAGTTGAGAGCTACTTATGAGATATGAA 329
Qy      84  ThrValHisLeuValMetGluLeuCysGluGlyGlyGluLeuPheGlyArgIleValAla 103
Db      330  GCAGTTTCATCTTGTTCATGGAGCTATGTGAAGTGGGAGTATTTGATAGAATTTGAGCT 389
Qy      104  ArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValVal 123
Db      390  AGAGGGCATTAACAGTGAAGAGCTGCAGCTGGGTGGCCAGAACTGTTGCAGAGGTTGTA 449
Qy      124  ArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPhe 143
Db      450  AGGATGTGTCATGCTAATGGGGTCATGCATAGAGACTTGAACCTTGAGAAATTTCTGTTT 509
Qy      144  AlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPhe 163
Db      510  GCTAATAAGAAAGAGCATTTGCTCTCAAGGCCATCGATTTTGGCCTATCTGTCTTTTTC 569
Qy      164  LysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluVal 183
Db      570  AAGCCTGTGTGAAGATTTCTCTGAGATTGTGGGAAGTCCATACATGACACAGAGGTG 629
Qy      184  LeuLysArgAsnTyrGlyProGluValAspValTrpSerAlaGlyValIleLeuTyrIle 203
Db      630  TTGAAGCGGAGTTATGGACCAAGAGTGTATTTGGAGTGGTGTGCTCATCTCTTATAT 689
Qy      204  LeuLeuCysGlyValProPheTrpAla 213
Db      690  TTGTTATGTGGGTTCTCTCCATTTTGGGCT 719

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RESULT 9
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LOCUS SCQGLB2041E01.g LB2 Saccharum officinarum cDNA clone SCQGLB2041E01
DEFINITION 5', mRNA sequence.
ACCESSION CA264357
VERSION CA264357.1 GI:35959325
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

```

clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

1 (bases 1 to 711)

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: 041 row: E column: 01

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1..711

FEATURES

source

/organism="Saccharum officinarum"

/mol_type="mRNA"

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/clone="SCQGLB2041E01"

/lab_host="DH10B"

/clone_lib="LB2"

/note="Organ: Lateral buds from plants adult plants growing in greenhouse; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [lateral buds from plants adult plants growing in greenhouse]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucst.lad.ic.unicamp.br/public>"

ORIGIN

Alignment Scores:

Pred. No.: 8,31e-109 Length: 711
Score: 1005.00 Matches: 192
Percent Similarity: 87.76% Conservative: 16
Best Local Similarity: 81.01% Mismatches: 29
Query Match: 70.82% Indels: 0
DB: 6 Gaps: 0

US-08-989-881-2 (1-274) x CA264357 (1-711)

Qy 31 ArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArgLysLeuArgThrAla 50
Db 1 CCGCGCTCAGGGAGGCGCTGGCCCTGCAAGTCCATCTCAAGAAAGAGCTCGCACCC 60
Qy 51 ValAspValGluAspValArgArgGluValThrIleMetSerThrLeuProGluHisPro 70
Db 61 GTTGACATCGAGGAGCTGCGCGGGAGGTGGAGATCATGCCACCTCCCAAGCACCC 120
Qy 71 AsnValValLysLeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGlu 90
Db 121 AACGTGTCGTCAGGAGCACCTTACGAGGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 180
Qy 91 LeuCysGluGlyGlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArg 110
Db 181 CTCTGTGAGGGCGGGAGCTCTTCGACCGCATCGTGGCGGGGACATCTACACTGAGGCG 240
Qy 111 AlaAlaAlaThrValAlaArgThrIleAlaGluValValAlaArgMetCysHisValAsnGly 130
Db 241 GCTGCGCTTGGTCACAGGCACTATCTGCGAGGTCTGTCAGATGTGTCATAGCATGGA 300
Qy 131 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaAsnLysGluAsnSer 150
Db 301 GTGATGTCAGGGATCTCAACACCAAGAAATTTCTTTGTTGGCAACAAGAAATTCAGCA 360

Qy 151 AlaleuLysAlaIleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPheThr 170
Db 361 GCCCTTAAGGCCATTGATTTGGCTCTGTGTATTTTCTACTCAGGCGAAACGGTTACT 420
Qy 171 GluIleValGlySerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyPro 190
Db 421 GAGATTGTTGGAAGTCTTATTACATGGCTCCAGAGGTCTTAAGAGAAATATATGCCCA 480
Qy 191 GluValAspValTrpSerAlaGlyValIleLeuTyrIleLeuLysGlyValProPro 210
Db 481 GAGGTTGATGTNTGAGTGCAGGAGTGATTCTGTACATTTCTTCTTTGTGTGCTCCTCCA 540
Qy 211 PheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuArgGlyValLeuAspPhe 230
Db 541 TTCGGGCGAAGAACGGAACAGGGGTGTNGCTCAGGCAATTTATCCGATCTGCCATGATTTC 600
Qy 231 LysArgAspProTrpSerGlnIleSerGluSerAlaLysSerLeuValLysGlnMetLeu 250
Db 601 AAAGAGATCCATGCGCAAGGGTCTCTGGATACGCCCAAGAACTTGTCCAGAGGAATGCTC 660
Qy 251 GluProAspSerThrLysArgLeuThrAlaGlnGlnValLeuAspHisPro 267
Db 661 AATCCGGANTCCAAACGACGATGACAGCTCAGCAAGTGTGTGATCACCCA 711

RESULT 10
CK281626 982 bp mRNA linear EST 02-AUG-2004
LOCUS EST744348 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMA557 5',
end, mRNA sequence.
CK281626
CK281626.1 GI:39852434
VERSION EST.
KEYWORDS Nicotiana benthamiana
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE asterids; lamids; Solanales; Solanaceae; Nicotiana.
JOURNAL 1 (bases 1 to 982)
COMMENT Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST744346 EST744347 EST744349
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

1..982

/organism="Nicotiana benthamiana"

/mol_type="mRNA"

/db_xref="taxon:4100"

/clone="NBMA557"

/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"

/lab_host="DH10B-Tona"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/notes=vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

supplier: RNA was isolated from Nicotiana benthamiana

tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomato 12 hr;

Xanthomonas campestris pv campestris 12 hr;

Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas

campestris pv vesicatoria 18hr). RNA was isolated from

these tissues and pooled in approximately equal molar

amounts."

ORIGIN

Alignment Scores:
Pred. No.: 1,73e-108 Length: 982
Score: 1004.00 Matches: 185
Percent Similarity: 86.59% Conservative: 28
Best Local Similarity: 75.20% Mismatches: 33
Query Match: 70.75% Indels: 0
DB: 7 Gaps: 0

US-08-989-881-2 (1-274) x CK281626 (1-982)

Qy 4 GlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGluPheGly 23
Db 238 AAATCGAATATCGAGGAATATATCTAGTTGATAGAGATTAGGAAGAGTGAATTCGGA 297
Qy 24 IleThrTyrLeuGlySerAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSer 43
Db 298 ATAACCTACCTCTGTACCGATCGTAACAGCAGTGAATTTGGCTTGAAGTCAATTCG 357
Qy 44 LysArgLysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMet 63
Db 358 AAGCGGAAACTTAGAACATCTGTGTATAGAGGATGTAAGCGAGAGAGTGGCGATAATG 417
Qy 64 SerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGlu 83
Db 418 AAGCATTTCCGCTAGATTGAGCATTTGAGATTCAGAGAGCTGTGAGGATGAGAT 477
Qy 84 ThrValHisLeuValMetGluLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyValAla 103
Db 478 CGGGTGCAATTTGGTATGAGTTGTGCGAAGCGCGGAGCTGTTCATAGGATAGTGGCG 537
Qy 104 ArgGlyHisTyrThrGluArgAlaAlaThrValAlaArgThrIleAlaGluValVal 123
Db 538 CGGGGGCATTCACCGAGCGTCTGCTCGCGGTGTCTCGGAGCGGTGTGGAAGTGGTG 597
Qy 124 ArgMetCysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPhe 143
Db 598 CAGCTTTGTATAGAGTGTGTGATTCATGAGACTTGAACCTGAGAACCTTTTGT 657
Qy 144 AlaAsnLysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPhe 163
Db 658 GCTAATAAAAGAGAAATTCGCACCTTAAGGCTATTGATTTGGTTTGTCCATATCTTC 717
Qy 164 LysProGlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluVal 183
Db 718 CAGCCAGGTGAGAGTCTTCTGAAATTTGTGAAGCCCTTATATATGCTCTCAGGCTG 777
Qy 184 LeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeuTyrIle 203
Db 778 CTCAGCGGAACTATGGACCAGAAATAGATATATGAGGTGCGAGGAGTCAATATATAT 837
Qy 204 LeuLeuGlyValProPheTrpAlaGluThrGluGlnGlyValAlaLeuAlaIle 223
Db 838 TTGTTATGTGGAGTCTCTCCCTTTGGGCTGAATCTGAACAAGGTGTTGCTCAGGCGATC 897
Qy 224 LeuArgGlyValLeuAspPheLysArgAspProTyrSerGlnIleSerGluSerAlaLys 243
Db 898 TTACGTGGAGCAATAGATTTCAGCGGTGACCCCTGGCCGAGTATTTCAGAGACTCTCTACA 957
Qy 244 SerLeuValLysGlnMet 249
Db 958 AATCTTTGACACAATG 975

RESULT 11
CK297575
LOCUS EST760289 889 bp mRNA linear EST 02-AUG-2004
DEFINITION EST760289 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMD981 5'
end, mRNA sequence.
ACCESSION CK297575
VERSION CK297575.1 GI:39884099
KEYWORDS EST.

SOURCE
ORGANISMNicotiana benthamiana
Nicotiana benthamianaEukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE

1 (bases 1 to 889)

AUTHORS

Buell, C.R., Hart, A., Ziemann, V., Karamycheva, S.A., Day, B.,

TITLE

Generation of EST sequences from Nicotiana benthamiana

JOURNAL

Unpublished (2003)

COMMENT

Other ESTs: EST760290

Contact: Robin Buell

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9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@igr.org

Clones can be requested from the University of Arizona Genomics

Institute via <http://genome.arizona.edu/orders/>

Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

Location/Qualifiers

source

1..889

/organism="Nicotiana benthamiana"

/mol_type="mRNA"

/db_xref="taxon:4100"

/clone="NBMD981"

/tissue_type="abiotic and biotic stress-treated leaves,

callus tissue and root tissue"

/lab_host="DH10B-Tona"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

supplier: RNA was isolated from Nicotiana benthamiana

tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomato 12 hr;

Xanthomonas campestris pv campestris 12 hr, 18hr;

Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas

campestris pv vesicatoria 18hr). RNA was isolated from

these tissues and pooled in approximately equal molar

amounts."

ORIGIN

Alignment Scores:

Pred. No.: 4,05e-102 Length: 889
Score: 950.00 Matches: 175
Percent Similarity: 87.39% Conservative: 26
Best Local Similarity: 76.09% Mismatches: 29
Query Match: 66.95% Indels: 0
DB: 7 Gaps: 0

US-08-989-881-2 (1-274) x CK297575 (1-889)

Qy 4 GlnThrGlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGluPheGly 23
Db 199 AAATCGAATATCGAGGAATATATCTAGTTGATAGAGATTAGGAAGAGTGAATTCGGA 258
Qy 24 IleThrTyrLeuGlySerAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSer 43
Db 259 ATAACCTACCTCTGTACCGATCGTAACAGCAGTGAATTTGGCTTGAAGTCAATTCG 318
Qy 44 LysArgLysLeuArgThrAlaValAspValGluAspValArgGluValThrIleMet 63
Db 319 AAGCGGAACTTAGAACATCTGTGTATAGAGGATGTAAGCGAGAGAGTGGCGATAATG 378
Qy 64 SerThrLeuProGluHisProAsnValValLysLeuLysAlaThrTyrGluAspAsnGlu 83
Db 379 AAGCATTTCCGCTAGATTGAGCATTTGAGATTCAGAGAGCTGTGAGGATGAGAT 438
Qy 84 ThrValHisLeuValMetGluLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyValAla 103
Db 439 CGGGTGCAATTTGGTATGAGTGTGCGAAGCGCGGAGCTGTTCGATAGGATAGTGGCG 498
Qy 104 ArgGlyHisTyrThrGluArgAlaAlaThrValAlaAlaThrIleAlaGluValVal 123


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|||||
499 CGGGGGATTACACGGAGCGTGCCTCGCGCTCATCGCGAGCGTTGTGGAAGTGGT 558
|||||
124 ArgMetCysHisValAsnGlyValMetHisArgAspLeuLeuPheProGluAsnPheLeuPhe 143
|||||
559 CAGCTTTGTCATAGAATGGTGTGATCATCGAGACTTGAACTGAGAACTTTTGT 618
|||||
144 AlaAsnLysLysGluAsnSerAlaLeuLysAlaLeuAspPheGlyLeuSerValLeuPhe 163
|||||
619 GCTAATAAAAGAGAAATTCGCCACTTAAAGGCTATTGATTTGGTTGTCTCATATTC 678
|||||
164 LysProGlyGluArgPheThrGluLeuValGlySerProTyrTyrMetAlaProGluVal 183
|||||
679 CAGCAGGTGAGAGGTTTCTGAAATTTGGAAGCCCTTATTATATGCGCTCTGAGGTG 738
|||||
184 LeuLysArgAsnTyrGlyProGluValAspValTyrSerAlaGlyValIleLeuTyrIle 203
|||||
739 CTCAGCGCAACTATGACCAAGAAATAGATATATGAGTGCAGGAGTCAATTATGAT 798
|||||
204 LeuLeuCysGlyValProPheTyrAlaGluThrGluGlnGlyValAlaLeuAlaIle 223
|||||
799 TTGTTATGTGGAGTTCCTCCCTTTGGGCTGAATCTGAACAAGGTGTGCTCAGGCCATC 858
|||||
224 LeuArgGlyValLeuAspPheLysArgAsp 233
|||||
859 TTACGTGAGCAATAGATTTCAAGCGTGAA 888
|||||

RESULT 12
CB894498 864 bp mRNA linear EST 24-APR-2003
LOCUS CB894498
DEFINITION CB894498 HOGA Medicago truncatula cDNA clone HOGA-31K18, mRNA
sequence.
ACCESSION CB894498
VERSION CB894498.1 GI:30101667
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 864)
Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S.,
Utterback, T., Cho, J., and Fraser, C.M.
ESTs from roots of Medicago truncatula treated with
oligogalacturonides of DP 6-20
Unpublished (2001)
Contact: Michael G. Hahn
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602-4712, USA
Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@ccrc.uga.edu
TIGR sequence name: MTWDT69TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA gTg GAT CC).
Location/Qualifiers
1..864
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3890"
/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at 26 C
with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
/clone_lib="HOGA"
/note="Vector: pluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from

```

Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in SOLR cells."

ORIGIN

Alignment Scores: 1.53e-101 Length: 864
Pred. No.: 945.00 Matches: 176
Score: 89.55% Conservative: 21
Percent Similarity: 80.00% Mismatches: 23
Best Local Similarity: 66.60% Indels: 0
Query Match: 6 Gaps: 0
DB:

US-08-989-881-2 (1-274) x CB894498 (1-864)

Qy 55 AspValArgArgGluValThrIleMetSerThrLeuProGluHisProAsnValValLys 74
Db 1 GATGTTGCGCGTGAAGTTGCTATCATCGCCATTGGCCCAAGAGTTTCGAGTATTGTGCACG 60
Qy 75 LeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGluLeuLysGluGly 94
Db 61 CTTGCTGAAGCGTGTGAGGATGATATGCTGTGTTTCATCTTGTCTATGAGAGCTTTGTGAAGGT 120
Qy 95 GlyGluLeuPheGlyArgIleValAlaAtgGlyHisTyrThrGluArgAlaAlaAlaThr 114
Db 121 GGGGAGCTTTTTCATCGGATTTGTGTAGAGGACATTATACGAGAGAGCGGCTCGCGCG 180
Qy 115 ValAlaArgThrIleAlaGluValAlaArgMetCysHisValAsnGlyValMetHisArg 134
Db 181 GTTGGGAGGACGATTGTGGAGGTTGTGCACCTTTGTCATAAGCATGGGTTATTTCATCGC 240
Qy 135 AspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAla 154
Db 241 GATCTTAAAGCCGGAGAAATTTCTTTTGGCAATTAAGAAGGAGAAATTCGCCACTTTAAGGCT 300
Qy 155 IleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPheThrGluIleValGly 174
Db 301 ATTGATTTTGGGTGTCTATTCTTTTAAACCAGGTGAGAAATCTCAGAAATTTGTGGA 360
Qy 175 SerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyProGluValAspVal 194
Db 361 AGTCCATATTACATGGCTCCAGAGGTGCTCAAGCGGAACTATGGACCTGAAATAGATATA 420
Qy 195 TrpSerAlaGlyValIleLeuTyrIleLeuLysCysGlyValProPheThrAlaGlu 214
Db 421 TGGAGTGCAGGAGTGATCTTATATCTTATTGTGCGGTGTTCCCGCTTTTGGGCTGAA 480
Qy 215 ThrGluGlnGlyValAlaLeuAlaIleLeuArgGlyValLeuAspPheLysArgAspPro 234
Db 481 TCTGAGCAAGGAGTTTGCACCAAGCTATTCTTCGAGGCGCTTATAGATTTCAACCGGAACT 540
Qy 235 TrpSerGlnIleSerGluSerAlaLysSerLeuValLysGlnMetLeuGluProAspSer 254
Db 541 TGGCCCAAGTATTCTGAAAGTGTCTAAAGTCTTTGTTAAGCAATTTTGGAAACAGACCT 600
Qy 255 ThrLysArgLeuThrAlaGlnGlnValLeuAspHisProTyrIleGlnAsnAlaLysLys 274
Db 601 AAGCTTCGATTAAACGCCCAACAAAGTCTTTGAGCATCTCTTGGCTCCAAAATGCTAAGAAG 660

RESULT 13

CB894498 688 bp mRNA linear EST 26-SEP-2003
LOCUS CB894498
DEFINITION CB894498 HOGA Medicago truncatula cDNA clone SCAGLB2046H03
5', mRNA sequence.
ACCESSION CB894498
VERSION CB894498.1 GI:35965079
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

ORIGIN

Alignment Scores:
Pred. No.: 4,29e-101 Length: 679
Score: 940.00 Matches: 176
Percent Similarity: 88.34% Conservative: 21
Best Local Similarity: 78.92% Mismatches: 25
Query Match: 66.24% Indels: 1
DB: 5 Gaps: 0

US-08-989-881-2 (1-274) x BQ148394 (1-679)

Qy 6 GlnIleSerAspLysTyrIleLeuGlyArgGluLeuGlyArgGlyGluPheGlyIleThr 25
Db 11 GAGATATTACAAATTCGAATTTAGGGAGAGAAATTTAGGAGAGAGAAATTTGGAATAACG 70
Qy 26 TyrLeuGlyThrAspArgGluThrArgGluAlaLeuAlaCysLysSerIleSerLysArg 45
Db 71 TATTATGTAAGATAGAGAACGGGAGAGGAAATTTAGCTTGTAAATCGATTTCAAGGAT 130
Qy 46 LysLeuArgThrAlaValAspValGluAspValArgArgGluValThrIleMetSerThr 65
Db 131 AAGCTAAGACACGCGATTTGATATTCAGATGTTAGACAGAGAGCTTGAATATGAGGCAT 190
Qy 66 LeuProGluHisProAsnValLysLeuLysAlaThrTyrGluAspAsnGluThrVal 85
Db 191 TTACCTAAACATCTTAAATATTTGTTTACGTTGAAGGATCTTTATGAAGATGATTAATGTT 250
Qy 86 HisLeuValMetGluLeuGlyGlyGluLeuPheGlyArgIleValAlaArgGly 105
Db 251 CATCTTGTATGGAGCTTTGTGAAGTGTGAGCTTTTGTGATCGGATTTGCTTAAGGGA 310
Qy 106 HisTyrThrGluArgAlaAlaAlaThrValAlaArgThrIleAlaGluValValArgMet 125
Db 311 CATTATACCGAACG 370
Qy 126 CysHisValAsnGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAlaLeu 145
Db 371 TGCCACGAACATGGTGTGATGATCGGATCTCAAAACCGAGAACTTTTGTGTCGAAC 430
Qy 146 LysLysGluAsnSerAlaLeuLysAlaIleAspPheGlyLeuSerValLeuPheLysPro 165
Db 431 AAGAAGGAACATCACCTTTGAAAGCTATTGACTTTGTTGTTGTTGTTGTTGTTGTTGTT 490
Qy 166 GlyGluArgPheThrGluIleValGlySerProTyrTyrMetAlaProGluValLeuLys 185
Db 491 GGTGATAAATTTAAGAGATAGTTGGAGTCCATATTACATGCGCCCTGAAAGTATTGAAG 550
Qy 186 ArgAsnTyrGlyProGluValAspValTrpSerAla-GlyValIleLeuTyrIleLeuLe 205
Db 551 AGAAATATGCCCCCTGAAATAGATATCTGGAGTCCCGAGTAATCTTTACATCTTACT 610
Qy 205 uCysGlyValProProPheTpaAlaGluThrGluGlnGlyValAlaLeuAlaIleLeuAr 225
Db 611 TTGGTATCTCTCTCTTTTGGGCANAACTGAGCAGGGAATTTGCTCAAGCAATTTATAG 670
Qy 225 gGlyVal 227
Db 671 ATCCGTT 677

RESULT 15

CV470355 LOCUS 914 bp mRNA linear EST 01-OCT-2004
DEFINITION 43200.1 Common 'Scab'-Challenged Tubers Solanum tuberosum cDNA clone
43200 5', mRNA sequence.
ACCESSION CV470355
VERSION CV470355.1 GI:53695131
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

FEATURES

Location/Qualifiers
1..914
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clones="43200"
/tissue_type="Tubers"
/lab_host="XL10-Gold"
/clone_lib="Common Scab-Challenged Tubers"
/notes="vector: pBluescript II SK(+); Site_1: EcoRI; Site_2: XhoI; supplier: Pathogen-challenge series. Tubers from pathogen-free Solanum tuberosum var. Shepody, clone 1756, were inoculated with Streptomyces scabei EF-35, by applying 1 ml of a spore stock (OD650 = 0.7). Tubers were placed in trays of sand and watered from the bottom for the remainder of the experiment. Inoculated tubers were sampled at 2 days, 1 week, 2 weeks and 4 weeks post-infection. Harvested tubers were washed in distilled water, blotted dry, cut into small pieces and frozen in liquid nitrogen. RNA was isolated from each sample collection, pooled and used for cDNA library construction."

ORIGIN

Alignment Scores:
Pred. No.: 9,87e-101 Length: 914
Score: 938.50 Matches: 195
Percent Similarity: 81.34% Conservative: 23
Best Local Similarity: 72.76% Mismatches: 42
Query Match: 66.14% Indels: 9
DB: 7 Gaps: 2

US-08-989-881-2 (1-274) x CV470355 (1-914)

Qy 15 ArgGluLeuGlyArgGlyGluPheGlyIleThrTyrLeuCysThrAspArgGluThrArg 34
Db 1 AGAGAGTTAGGAGGGGGAATC-GGGATAACTTTACCTTTGTATAGATCGTAGCAGTAGG 59
Qy 35 GluAlaLeuAlaCysLysSerIleSerLysArgLysLeuArgThrAlaValAspValGlu 54
Db 60 GAACCTTTGGCTTGTAAAGTCGATTTCCGAAACGGGAAGTTACGACAGAGTGATGTGGAG 119
Qy 55 AspValArgArgGluValThrIleMetSerThrLeuProGluHisProAsnValLys 74
Db 120 GATGTAGGAGAGAGAGTGGCAATTTATCAAGCATTTGCCACAGAAATTCAGATTTGTGAGT 179
Qy 75 LeuLysAlaThrTyrGluAspAsnGluThrValHisLeuValMetGluLeuCysGluGly 94
Db 180 TTTAAGGAAGCGTGTGAGGATGAAATGCTGTTTCATTTGGTGTGGAACATATGTGAAGGT 239
Qy 95 GlyGluLeuPheGlyArgIleValAlaArgGlyHisTyrThrGluArgAlaAlaAlaThr 114
Db 240 GGTGAGCTGTTTGTATAGGATCGTTGCTAGGGGGCATTTATCTGAACGAGCAGCTGCTGCT 299
Qy 115 ValAlaArgThrIleAlaGluValValArgMetCysHisValAsnGlyValMetHisArg 134
Db 300 GTTACACGACGATTTGTGGAGTTGTGCAGCTTTGTCCAAACATGAGTGATTCATAGA 359
Qy 135 AspLeuLysProGluAsnPheLeuPheAlaAsnLysLysGluAsnSerAlaLeuLysAla 154

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Db      360 GATTGAGCCCGAGACACTTTTGTGCTAATAAGAGGAAATTCACCTCTTAAGCA 419
Qy      155 IleAspPheGlyLeuSerValLeuPheLysProGlyGluArgPheThrGluIleValGly 174
Db      420 ATTGAATTTGGCTTGTCAATCTTCAAGCCAGGTGAGAAGTTCTCTGAATAGTTGGA 479
Qy      175 SerProTyrTyrMetAlaProGluValLeuLysArgAsnTyrGlyProGluValAspVal 194
Db      480 AGTCCATATTATATGGCTCTGAGGTCTCAACGAAACTATGGACCAGAAATAGATATA 539
Qy      195 TrpSerAlaGlyValIleLeuTyrIleLeuLeuCysGlyValProPheTrpAlaGlu 214
Db      540 TGCAGTGCAGGAGTCATTTTATATATATTTTCTATGTGGGTCTCTCCCTTTTGGCCGAA 599
Qy      215 ThrGluGlnGlyValAla-LeuAlaIleLeuArgGlyValLeuAspPheLys-ArgAsp- 233
Db      600 TCTGAACAAGGTGTGCCCCAAGCCATTTTACGTGGGGCAATAGATTTCAAGCGGGAAC 659
Qy      234 ProTrpSerGlnIleSerGluSerAla---LysSerLeuValLysGlnMetLeuGluPro 252
Db      660 CCTGGCCCAAGTATTTCAAGAGGGTGCTAAATACTTTGCTCAGGGCAATGTAAGCAGG 719
Qy      253 AspSerThrLysArgLeuThr-----AlaGlnGlnValLeuAspHisPro-TrpIle-G 270
Db      720 CAAGATCCAAAGGCTTCGACTGCACTGCAAAAGCAAGTACTTTGAGCACCCCTTTGGGTTC 779
Qy      270 InAsnAlaLysLys 274
Db      780 AAAATGCTAAGAAA 793
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Search completed: October 14, 2005, 23:21:48
Job time : 3529 secs